

FIGURE 1

GGCATCTGCCCGAGGAGACCACGCTCCTGGAGCTCTGCTGTCTTCTCAGGGAGACTCTGAGG
CTCTGTTGAGAATCATGCTTTGGAGGCAGCTCATCTATTGGCAACTGCTGGCTTTGTTTTTC
CTCCCTTTTTGCCTGTGTCAAGATGAATACATGGAGTCTCCACAAACCGGAGGACTACCCCC
AGACTGCAGTAAGTGTTGTCTATGGAGACTACAGCTTTCGAGGCTACCAAGCCCCCTGGGC
CACCGGGCCCTCCTGGCATTCCAGGAAACCATGGAACAAATGGCAACAAATGGAGCCATGGT
CATGAAGGAGCCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGCCCTCGAGGGGAGCGGGG
GCAGCATGGCCCCAAAGGAGAGAAGGGCTACCCGGGGATTCCACCAGAACTTCAGATTGCAT
TCATGGCTTCTCTGGCAACCCACTTCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTT
GAGACCAACATTGGAACACTTCTTTGATGTCTATGACTGGTAGATTGGGGCCCCAGTATCAGG
TGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGATGTTGAGGAAGTGTATGTGTACC
TTATGCACAATGGCAACACAGCTTCTCAGCATGTACAGCTATGAAATGAAGGGCAAAATCAGAT
ACATCCAGCAATCATGCTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTGCGAATGGG
CAATGGCGCTCTCCATGGGGACCACCAACGCTTCTCCACCTTTGCAGGATTCCTGCTCTTTG
AACTAAGTAAATATATGACTAGATAGCTCCACTTTGGGGAAGACTTGTAGCTGAGCTGAT
TTGTTACGATCTGAGGAACATTAAGTTGAGGGTTTACATTTGCTGTATTCAAAAAATTATT
GGTTGCAATGTTGTTACGCTACAGGTACACCAATAATGTTGGACAATTTCAGGGGCTCAGAA
GAATCAACCACAAAATAGTCTTCTCAGATGACCTTGACTAATATACTCAGCATCTTTATCAC
TCTTTCCTTGGCACCTAAAGATAATTCTCCTCTGACGCAGGTTGGAATAATTTTTTCTAT
CACAGAAGTCATTTGCAAGAATTTTGACTACTCTGCTTTTAATTTAATACCAGTTTTCAGG
AACCCCTGAAGTTTTAAGTTCATTATTCTTTATAACATTTGAGAGAATCGGATGTAGTGATA
TGACAGGGCTGGGGCAAGAACAGGGGCACTAGCTGCCTTATTAGCTAATTTAGTGCCCTCCG
TGTTGAGCTTAGCCCTTGACCCCTTCCCTTTTGATCCACAAAATACATTAAAACTCTGAATTC
ACATACAATGCTATTTTAAAGTCAATAGATTTTAGCTATAAAGTGCTTGACCAGTAATGTGG
TTGTAATTTTGTGATGTTCCCCACATCGCCCCAACTTCGGATGTGGGGTCAGGAGGTTG
AGGTTCACTATTAACAAATGTCATAAATATCTCATAGAGGTACAGTGCCAATAGATATTCAA
ATGTTGCATGTTGACCAGAGGGATTTTATATCTGAAGAACATACACTATTAATAAATACCTT
AGAGAAAGATTTTGACCTGGCTTTAGATAAACTGTGGCAAGAAAATGTAATGAGCAATAT
ATGGAATAAACACACCTTTGTTAAAGATAAAAAAAA

FIGURE 2

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44686

><subunit 1 of 1, 246 aa, 1 stop

><MW: 26994, pI: 6.43, NX(S/T): 0

MLWRQLIYWQLLALFFLPCLCQDEYMESPQTGGLPPDCSKCCHGDYSFRGYQGPPGPPGPP
GIPGNHGNNGNNGATGHEGAKGEKGDGDLGPRGERGQHGPKEKGYPGIPPELQIAFMASL
ATHFSNQNSGIIFSSVETNIGNFFDVTGRFGAPVSGVYFFTFSMMKHEDVEEVYVYLMHNG
NTVFSMYSYEMKGKSDTSSNHA VLK LAKGDEVWL RMGN GALHGDHQR FSTFAGFL LFETK

Important features of the protein:

Signal peptide:

amino acids 1-22

Motif name: Clq domain signature.

amino acids 137-167

Clq domain proteins.

amino acids 135-169, 202-221, 235-244, 57-91, 60-94, 54-88, 81-114, 78-111, 63-96, 51-84, 45-78, 48-81, 33-66, 66-99 and 42-75

FIGURE 3

GAGAGAATAGCTACAGATTCTCCATCCTCAGTCTTTGCAAGGCGACAGCTGTGCCAGCCGGG
CTCTGGCAGGCTCCTGGCAGCATGGCAGTGAAGCTTGGGACCCTCCTGCTGGCCCTTGCCCT
GGGCTGGCCAGCCAGCCTCTGCCCCGCCGAAGCTGCTGGTGTTCCTGCTGGATGGTTCCT
GCTCAGACTACATCAGTGATGAGGCGCTGGAGTCATTGCCTGGTTTCAAAGAGATTGTGAGC
AGGGGAGTAAAAGTGGATTACTTGGACTCCAGACTTCCCTAGTCTCTCGTATCCCAATTATTA
TACCCTAATGACTGGCCGCCATTGTGAAGTCCATCAGATGATCGGGAACACATGTGGGACC
CCACCACCAACAAGTCCTTTGACATTGGCGTCAACAAAGACAGCCTAATGCCTCTCTGGTG
AATGGATCAGAACCTCTGTGGGTCACTCTGACCAAGGCCAAAAGGAAGGTCTACATGTACTA
CTGGCCAGGCTGTGAGGTTGAGATTCTGGGTGTGAGCCACCTACTGCCTAGAATATAAAA
ATGTCCCAACGGATATCAATTTTGCCAATGCAGTCAGCGATGCTCTTGACTCCTTCAAGAGT
GGCCGGGCGACCTGGCAGCCATATACCATGAGCGCATTGACGTGGAAGGCCACCACTACGG
GCCTGCATCTCCGCAGAGAAAGATGCCCTCAAGGCTGTAGACACTGTCTGAAGTACATGA
CCAAGTGGATCCAGGAGCGGGCCTGCAGGACCGCCTGAACGTCATTATTTCTCGGATCAC
GGAATGACCGACATTTTCTGGATGGACAAAGTGATTGAGCTGAATAAGTACATCAGCCTGAA
TGACCTGCAGCAAGTGAAGGACCGCGGGCCTGTTGTGAGCCTTTGGCCGGCCCCCTGGGAAAC
ACTCTGAGATATATAACAACTGAGCACAGTGGAACACATGACTGTCTACGAGAAAGAAGCC
ATCCCAAGCAGGTTCATTACAAGAAAGGAAAGTTGTCTCTCCTTTGACTTTAGTGGCTGA
TGAAGGCTGGTTCATAACTGAGAATCGAGAGATGCTTCCGTTTTGGATGAACAGCACCGGCA
GGCGGAAGGTTGGCAGCGTGGATGGCACGGCTACGACAACGAGCTCATGGACATGCGGGGC
ATCTTCTGGCCTTCGGACCTGATTTCAAATCCAACCTTCAGAGCTGCTCCTATCAGGTGCGT
GGACGTCTACAATGTGATGTGCAATGTGGTGGGCATCACCCGCTGCCCAACAACGGATCCT
GGTCCAGGGTGATGTGCATGCTGAAGGGCCGCGCCGGCCTGCCCCGCTGTCTGGCCAGC
CACTGTGCCCTGGCACTGATTCTTCTCTCTGCTTGCATTAACTGATCATATTGCTTGCTC
AGAAAAAACACCATCAGCAAAGTGGGCCTCCAAGCCAGATGATTTTCATTTTATGTGTGA
ATAATAGCTTCATTAACACAATCAAGACCATGCACATTGTAATACATTATTCTTGATAAT
TCTATACATAAAAGTTCTACTTGTATAA

FIGURE 4

MAVKLGTLALLALGLAQPASARRKLLVFLLDGFRSDYISDEALES LPGFKEIVSRGVKVDY
LTPDFPSLSYPNYYTLMTGRHCEVHQMIGNYMWDPPTNKSFDIGVNKDSLMPLWWNGSEPLW
VTLTKAKRKVYMYWPGCEVEILGVRPTYCLEYKNVPTDINFANAVSDALDSFKSGRADLAA
IYHERIDVEGHHYGPASPQRKDALKAVDTVLKYMTKWIQERGLQDRNLNVIIFS DHGMTDIFW
MDKVIELNKYISLNDLQQVKDRGPVVS LWPAPGKHSEIYNKLSTVEHMTVYEKEAIPSRFYY
KKGKFVSPLTLVADEGWFITENREMLPFWMNSTGRREGWQRGWHGYDNE LMDMRGIFLAFGP
DFKSNFRAAPIRSVDVYNVMCNVVGITPLPNNGSWSRVCMCLKGRAGTAPPVWPSHCALALI
LLFLLA

Important features of the protein:

Signal peptide:

amino acids 1-22

N-glycosylation sites.

amino acids 100-104, 118-122, 341-345, 404-408

N-myristoylation sites.

amino acids 148-154, 365-371

Amidation site.

amino acids 343-347

FIGURE 5

GCCAGGTGTGCAGGCCGCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACC**ATGA**CGCTCCTCC
 CCGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCTCAGG
 GGGCACCCACACAGTCAGGTACCCACACTGCTACTGGCTGAGGAAGTCCCCCTCGGCCA
 GGCCCCCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTTGCCTGTAGCCCTGG
 TGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGCTACGACCCAG
 TGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCACCAGCGCTCCATCTCACC
 CTGGAGATACCGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTTCGCCGAGT
 GCCTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGCTGCGCTCAACTCCGTG
 CGGCTGCTCCAGAGCCTGCTGGTGTGCGCCGCCGGCCCTGCTCCCGCGACGGCTCGGGGCT
 CCCACACCTGGGGCCTTTGCCCTCCACACCGAGTTCATCCACGTCCCCGTGGCTGCACCT
 GCGTGTGCCCCGTTCACTG**TGA**CCGCCGAGGCCGTGGGGCCCCTAGACTGGACACGTGTGC
 TCCCCAGAGGGCACCCCCATTTATGTGTATTTATGTTATTTATATGCCTCCCCAACACT
 ACCCTTGGGGTCTGGGCATTCCCCGTGTCTGGAGGACAGCCCCCACTGTTCTCCTCATCTC
 CAGCCTCAGTAGTTGGGGGTAGAAGGAGCTCAGCACCTCTTCCAGCCCTTAAAGCTGCAGAA
 AAGGTGTCACACGGCTGCCTGTACCTTGGCTCCCTGTCTGCTCCCGGCTTCCCTTACCCTA
 TCACTGGCCTCAGCCCCGCGAGGCTGCCTCTTCCCAACCTCCTTGGAAGTACCCCTGTTTCT
 TAAACAATTATTTAAGTGTACGTGTATTATTAACTGATGAACACATCCCCAAAA

CCAGGTGTGCAGGCCGCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACC

FIGURE 6

MTLLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQAL
PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDYFPQKL
AFAECLCRGCIDARTGRETAALNSVRLQLSLLVLRRRPCSRDGSGLPTPGAFAFHTEFIHVP
VGCTCVLPRSV

Important features:

Signal peptide:

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 112-121

N-myristoylation sites.

amino acids 32-38, 55-61, 133-139

Leucine zipper pattern.

amino acids 3-25

Homologous region to IL-17.

amino acids 99-195

FIGURE 7

CGGCCAGGGCGCCGACAGCCCCGACCTCACCAGGAGAACAATGCAGCTCGGCACTGGGCTCCTG
CTGGCCGCGCTCCTGAGCCTGCAGCTGGCTGCAGCCGAAGCCATATGGTGTCACCAAGTGCAC
GGGCTTCGGAGGGTGCTCCCATGGATCCAGATGCCTGAGGGACTCCACCCACTGTGTCACCA
CTGCCACCCGGGTCTCAGCAACACCGAGGATTGCTCTGGTCACCAAGATGTGCCACATA
GGCTGCCCCGATATCCCCAGCCTGGGCCCTGGGCCCTACGTATCCATCGCTTGCTGCCAGAC
CAGCCTCTGCAACCATGACTGACGGCTGCCCTCCTCCAGGCCCCCGAGCGTCAGCCCCAC
AGCCCCACAGCCTGGCGCCAGGGCTCACGGCCGCCCTCCTCGAGACTGGCCAGCCCCAC
TCTCCCGGCCTCTGCAGCCACCGTCCAGCACCCTTGCTTAGGGAAGTCTGCGTGAGTGC
TTGCCTCAATCTGCTGCCGTCCAAGCCTGGGGCCCATCGTGCTGCCGCCCTTCAGGTCCC
GACCTCCCCACAATAAAATGTGATTGGATCGTGTGGTACAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 8

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77623

><subunit 1 of 1, 97 aa, 1 stop

><MW: 10160, pI: 6.56, NX(S/T): 0

MQLGTGLLLAAVLSLQLAAAEAIWCHQCTGFGGCSHGSRCLRDRSTHCVTATRVLSNTEDLP
LVTKMCHIGCPDIPSLGLGPYVSIACCQTSLCNHD

Important features of the protein:

Signal peptide:

amino acids 1-20

N-myristoylation sites.

amino acids 6-11 and 33-38

Prokaryotic membrane lipoprotein lipid attachment sites.

amino acids 24-34 and 78-88

FIGURE 9

CCAGGACCAGGGCGCACCGGCTCAGCCTCTCACTTGTGAGAGGCCGGGGAAGAGAAGCAAAG
CGCAACGGTGTGGTCCAAGCCGGGGCTTCTGCTTCGCCCTCTAGGACATACACGGGACCCCT
AACTTCAGTCCGCCCAAACCGCGACCCCTCGAAGTCTTGAACCTCAGCCCCGCACATCCACGGC
CGGCAAGGCGCGCGAGGCGAGGTCCCGGCCGAAGGCGATGCGCGCAGGGGGTTCGGGCAG
CTGGGCTCGGGCGCGGGGAGTAGGGCCCGCGAGGAGGCGAGGAGGCTGCATATTCAGAGTC
GCGGGCTGCGCCCTGGGGCAGAGGCGCCCTCGCTCCACGCAACACCTGCTGCTGCCACCGCG
CCGCGATGAGCGCGCTGGTCTCGCTGCTGCTGGGCGCGCGCTGCTCTGCGGCCACGGAGCC
TTCTGCCGCGCGTGGTCAGCGGCCAAAAGTGTGTTTTGCTGACTTCAAGCATCCCTGCTA
CAAAATGGCCTACTTCCATGAACTGTCCAGCCGAGTGAGCTTTCAGGAGGACGCGCTGGCTT
GTGAGAGTGAGGGAGGAGTCCCTCCTCAGCCTTGAGAATGAAGCAGAAGTTAATAGAG
AGCATGTTGCAAAACCTGACAAAACCCGGGACAGGGATTCTGATGGTGATTCTCGGATAGG
GCTTTGGAGGAATGGAGATGGGCAAAACATCTGGTGCTGCCAGATCTCTACCAAGTGGTCTG
ATGGAAGCAATTCACAGTACCGAAACTGGTACACAGATGAACCTTCTCGGGAAGTGAAGAG
TGTGTTGTGATGTATCACCACCAACTGCCAATCTGGCCTTGGGGGCTCCCTACCTTTACCA
TGGAATGATGACAGGTGTAACATGAAGCACAATATATTTGCAAGTATGAACAGAGATTA
ATCCAACAGCCCTGTAGAAAAGCCTTATCTTACAAATCAACAGGAGACACCCATCAGAAT
TGTGTTGTTACTGAAAGAGGTATAATTCCTAATCTAATTTATGTTGTTATACCAACAATACC
CTGCTCTTACTGTAAGTGGTGTGCTTTTGGAACTGTTGTTTCCAGATGCTGCATAAAAGAT
AAGGAAGAACAAAACCTAGTCCAACACAGTCTACACTGTGGATTTCAGAGGTACCGAAAA
GAAAGTGGCATGGAAGTATTAATAACTCATTGACTTGGTTCCAGAATTTGTAATTCGGATC
TGTATAAGGAATGGCATCAGAACAAATAGCTTGGAAATGGCTTGAATCACAAGGATCTGCAA
GATGAACGTGAAGCTCCCCCTTGAGGCAAAATATTAAGTAATTTTATATGTCTATTATTTTC
ATTTAAAGAATATGCTGTGCTAATAATGGAGTGAGACATGCTTATTTTGTAAGGATGAC
CCAAACTTCAAACCTCAAGCAATGAATGGACAATGCAGATAAAGTTGTTATCAACAGTCT
GGGAGTATGTGTGTAGAAAGCAATTCCTTTTATTTCTTTACCTTTTCATAAGTGTATCTA
GTCAATGTAATGTATATTGTATTGAAATTTACAGTGTCGCAAAAGTATTTTACCTTGCATAA
GTGTTTGATAAAAAATGAACGTGTTCTAATATTATTTTATGCGCATCTCATTTTTCAATACAT
GCTCTTTTGATTAAAGAACTTATTACTGTTGTCAACTGAATTCACACACACACAATAATAG
TACCATAGAAAAAGTTTGTTTTCTCGAAATAATTCATCTTTACGCTTCTCTGCTTTTGGTCA
ATGTCTAGGAAATCTCTTCAGAAATAAGAAGCTATTTTCAATTAAGTGTGATATAAAGCTCCTC
AAACATTTTACTTAGAGGCAAGGATTGTCTAATTTCAATTGTGCAAGACATGTGCCTTATAA
TTATTTTGTAGCTTAAATTAACAGATTTTGTAAATATGTAACCTTGTGTAATAGGTGCATAA
ACACTAATGCAGTCAATTTGAACAAAAGAAGTGACATACACAATAAATCATATGTCTTCA
ACGTTGCTTATATAATGAGAAGCAGCTCTCTGAGGGTTCTGAAATCAATGTGGTCCCTCTC
TTGCCCTACTAAACAAGATGGTGTTCGGGGTTTGGGATTGACACTGGAGGCGAGTAGTTGC
AAAGTTAGCTTAAGGTTTCCCTAGCTGTATTAGCCTCTGACTATATTAGTATACAAAGAGG
TCATGTGGTTGAGACCAGGTGAATAGTCACTATCAGTGTGGAGACAAGCACAGCACACAGAC
ATTTTAGGAAGGAAAGGAACACGAAATCGTGTGAAATGGGTTGGAACCCATCAGTGATCG
CATATTCAATTGATGAGGGTTTGTCTTGAGATAGAAATGGTGGCTCTTTCTGCTCTTATCTCC
TAGTTTCTTCAATGCTTACGCCTTGTTCTTCTCAAGAGAAAGTTGTAACCTCTCTGCTCTTCA
TATGTCCTGTGCTCCTTTTAAACAAATAAAGAGTCTTGTGTTCTGGGGGAAAAA
AAAAA

FIGURE 10

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA79230
><subunit 1 of 1, 273 aa, 1 stop
><MW: 30431, pI: 6.79, NX(S/T): 3
MSRVVSLLLGAALLCGHGAFCCR RVVSGQKVCFA DFKHPCYKMAYFHELSSRVSFQEARLACE
SEGGVLLSLENEAEQKLIESMLQNLTKPGTGISDGD F WIGLWRNGDGTSGACPDLYQWSDG
SNSQYRNWYTDEPSCGSEKCVVMYHQPTANFGLGGPYLYQWND DRCNMKHNYICKYEPEINP
TAPVEKPYLTNQPGDTHQNVVVTEAGIIPNLIYVVIPTIPLLLLILVAFGTCCFQMLHKSKG
RTKTSNPQSTLWISKSTRKESGMEV
```

Important features of the protein:

Signal peptide:

amino acids 1-21

Transmembrane domain:

amino acids 214-235

N-glycosylation sites.

amino acids 86-89 and 255-258

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 266-269

N-myristoylation sites.

amino acids 27-32, 66-71, 91-96, 93-98, 102-107, 109-114, 140-145
and 212-217

FIGURE 11

GGAGAGATGCGAGAGAGCACTGAGAGTGGAGTCCGGGGTCTGGTGGGGTGGTCTGTCTGCTCTGGCATGCCCTG
 CCACAGCCACTGGGCCCAGAGTTGCTCAGCCTGAAGTAGACACACCCTGGGTGCTGTGCGAGGCCGGCAGGTTGG
 GCGTGAAGGGACACAGCCGCTTGTGAATGTCTTTCTGGGCATTCCTATTGCCACGCCCATCTGGGCCCTGACC
 GGTCTCAGCCCCACACCCGACACAGCCCTGGAGGGTGTGCGGGATGCCAGCACTGCGCCCCAATGTGCTTAC
 AAGAGCTGGAGAGCATGAACAGCAGCAGATTGTCTCACAACGAAAAACAGCAGATCTTCTCGTTTCAGAGGACT
 GCCTGGTCTCAACGCTCTATAGCCAGCTGAGGTCCCGCAGGGTCCGGTAGGCCCGGTCTGGTATGGTCCATG
 GAGGCGCTCTGATAACTGGCGTGCACCTCCTACGATGGATCAGCTCTGGCTGCCATATGGGAGTGTGGTCCGTGG
 TTACAGTCCAGTACCGCTTGGGTCTTGGCTTCTTCAGCACTGGAGATGAGCATGCACCTGCCAACCCAGGGCT
 CTCTAGATGTGGTAGCTGCTTTGGCGTGGGTGCAAGAAAAACATCGCCCCCTTGGGGGTGACCTCAACTGTGTCA
 TGTCTTTGGTGGATCTCCGCTGGGAGCATCATCTCTGGCTGGTCTGTGCCAGTGGCTCGAGGGCTGTTC
 ACAGAGCATCACACAGATGGGGTCTACACACCCAGGGATCATCGACTCTACCCCTTGGCCCCCTAGCTCAGA
 AAATCGCAACACCTTGGCTGACGCTCCAGCTCCCGGGCTGAGATGTCAGTGCCTTCAGCAGAAAGAGGAG
 AAGAGCTGGTCTTAGCAAGAAGCTGAAAAATATCTATCTCTCACCCTGATGGCACTGTCTCCCCAAAA
 GCCCAGGAACTCCTGAAGGAGAAGCCCTTCACTCTGTGCCCTTCTCATGGGTGTCAACAACCATGAGTTCA
 GCTGGCTCATCCCCAGGGGCTGGGGTCTCTGGATACAATGGAGCAGATGAGCGGGAGGACATGCTGGCCATCT
 CAACACCGCTCTTGACCAATCTGGATGTGCCCCCTGAGATGATGCCACCTCATAGATGAATACCTAGGAAGCA
 ACTCGGAGCCACAACGCCAATGCCAGGCGTTCAGGAATTCATGGGTGACGTATTATCATGTCTTCCACCCGTCA
 GTTTTCAAGATACTCTCGAGATTCTGGAAGCCCTGTCTTTTCTATGAGTTCAGAGCATGACCCAGTCTTTTTC
 CGAAGATCAAACTGCTGGTGGTGAAGGCTGATCATGGGGCCGAGGGTGCTTTTGTGTTCCGAGGTCTCTCTCA
 TGGACAGAGCTCCCGCTGGCTGGCTTTCCAGAGGCCACAGAGGAGGAAGACCTTAAGCTCTACCATGAGTGGCC
 AGTGGAACCTTTGCCCGCCAGAGGGGACCCCAATAGCAAGGCTCTGCCCTCTGGCCCCAATTCAACCAAGTGG
 AACAAATCTTGAGATCAACCGAGTCCACAGTCCACAGCCGACAGAAATTCAGGAGGCTGGATGCAGTTCTGGTCAG
 AGACGCTCCCCAGCAAGATCAACCAATGGCACCAAGAGCAGAAGAACAGAGGCCACGAGGAGCTCTGAGGCC
 AGGCTGAACCTCTTGGCTGGGCCAACCACTCTTCAAGTGGTGAGAGTCCAGCAGAGCCCGCCGCTCTC
 CCGCTGTGAGACTTTAATCTCCACAGCCCTTAAAGTGTGCGGCGCTCTGTGACTGGATTTATGCTCTTTTGA
 ATGTCAGAGGCCGCGCTCCCACCTCTGGGGCATTTGACAAGTTCTGCCCTGAAAGTGGCTTCTGCTCTT
 CTTCTGTGGTAGGTTTAGCAGATTCTCTAGCTTCTGTGAGGACTCACTCCCGAGGAGCTTCCCTGCTCTCTC
 TGGGCTGTGGGGCCCGAGTCTGCGTCCATTAGAGCAGAGTCCACCGAGGCTAGCAGCGGTCTGTGCTGTCT
 CCCCCTCAGAGGAGCTCTTCAAAATGGGGATTAGCCTAACCCCACTCTGTACCCACACAGGATCGGGTGGGA
 CCTGGAGCTAGGGGGTGTGTTGCTGAGTGAGTGAGTGAACACAGAAATATGGAAATGGCAGCTGCTGAACTTGAAC
 CCAGAGCCTTCAGGTGCCAAAGCCATACTCAGGCCCCACCCGACATGTGCCACCTGGCCAGAAAGGTTGCATGCC
 AATGGCAGAGACTCGGATGGGAGAAGTCTGGGGGCCGACAGGGATCCAGCTAGGACAGACTTAGCCCTGAC
 TAAGGCTCAGACTAGGGCGGGAGGGGTCTCTCTCTCTGCTGCCAGTCTGGGCCCTGACACAAGACAACAG
 ATCCATCAGGGCCATGAGTGTACCCAGACCTGACCTCAACCAATTCAGCCCTTGACCTCAGGACGCTGGATG
 CCAGCTCCCGAGCCCACTGCGCGGTCTCCCTCCCTTCTGCTGTTGGGGAGACAGATTCTGGGAGGCTTCCAAG
 AGCACCCACCAAGACACAGCAGGAGCAGGCCAGGGGAGGGCATCTGGACCAGGGCATCCGTGGGGCTATTGTACAC
 GAGAAAAAGAGACCCACCATCTCGGGCTGCAAAAGGTGAAAAGCACCAGAGGTTTTCAGATGGAAGTGAGAG
 GTGACAGTGTGCTGGCAGCCTCACAGCCCTCGCTTGTCTCOCTGCCGCTCTGCTGGGCTGCCATTTGGCA
 GCACTTGAGGAGCCCTCAACCCGCGCTGCACTGTAGGAGCCCTTTCTGGGCTGGCCAAAGCCGGAGCCAGCT
 CCTCAGCTCTGCGGGGAGGTGCGGAGGGAGAGGGGCGGGCAGAAACCGGGGCTGCGCGCAGCGCTTGGCGGCCAG
 AGTGAATTGCGGGTGGGCTGGGCTCGCGGGGCCCACTCAGAGCAGCTGCGCGGCCAGGCACTGAGGGCT
 TAGCATCTGGGGCCAGCAGCTGCTGTCTCGATTCTCGTGGGCTTAGCTGCTCCCCGCGGGGAGGGCTCGG
 GACCTCAGCCCTCATGCTGCTGACCTCCCCACCCCGCTGGGCTGCTGTGCGGCGGAGCTCCCAAGGAG
 CGCCGCCCTCTCTCACAAGCGCCAGTCCCATCGACCCCAAGGGCTGAGGAGTGGGGTGCACAGCGCGGGA
 CTGGCAGGAGCTCCACTGCTGCCCCAGTCTGGATCACTGGGTGAAGCCAGTCTGGGCTCTGAGTCTGGTGG
 GGACTTGAAGAACTTTATGCTAGTCAAGGATTGTAATACACCGATGGGCATCTGTATCTAGCTCAAGGTT
 TGTAAACACACCAATCAGCACCTTGTGTAGTCTAGTCTGTTTGTGAATGCACCAATGCACACTCTGTATCTGGCT
 ACTCTGGTGGGACCTTGGAGAACCTTGTGTCCACACTCTGTATCTAGCTAATCTAGTGGGATGTGGAGAACCT
 TTGTGTCTAGCTCAGGATCTGTAAGCGCAACCAATCAGCAGCTGTCAAAACAGACCATGACTCTCTGTAATAA
 GGACCAATCAGCAGGATGTGGGTGGGCGGAGACAGAGAATAAAAGCAGGCTGCTGAGCCAGCAGTGAACACC
 CCTCGGCTCCCTCCACCGCGTGAAGCTTGTCTTCTGCTCTTTGCAATAAATCTTGCTACTGCCAAAA

FIGURE 12

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA79862

><subunit 1 of 1, 571 aa, 1 stop

><MW: 62282, pI: 5.56, NX(S/T): 1

MERAVRVESGVLGVVCLLLACPATATGPEVAQPEVDTTLGRVVRGRQGVGKGTDRLVNVFLG
IPFAQPLGLPDRFSAPHAPQWEGVRDASTAPPMCLQDVESMNSSRFVLNGKQQIFSVSEDC
LVNLNVYSPAIEVPAGSGRPVMVWVHGGALITGAATSYDGSALAAYGDVVVVTVQYRLGLVGLFF
STGDEHAPGNQGFLDVVAALRWVQENIAPFGDLNCVTVFSGSAGGSIISGLVLSFVAAGLF
HRAITQSGVITTPGIIDSHWPPLAQKIANTLACSSSSPAEMVQCLOQKEGEELVLSKKLKNT
IYPLTVDGTVPFKSPKELLKEKPFHSPVFLMGVNNHEFSWLIPRGWGLLDTMEQMSREDMLA
ISTPVLTSLDVPPPEMMPTVIDEYLGNSDAQAKCQAFQEFMGDVFINVPTVSFSRYLRDGS
PVFFYEFQHRPSSFAKIKPAWVKADHGAEGAFVFGGPFMLDESSRLAFPEATEEEKQLSLTM
MAQWTHFARTGDPNSKALPPWPQFNQAEQYLEINPVPRAGQKFREAWMQFWSETLPSKIQQW
HQQKQNRKAQEDL

Important features of the protein:

Signal peptide:

amino acids 1-27

Transmembrane domain:

amino acids 226-245

N-glycosylation site.

amino acids 105-109

N-myristoylation sites.

amino acids 10-16, 49-55, 62-68, 86-92, 150-156, 155-161,
162-168, 217-223, 227-233, 228-234, 232-238, 262-268, 357-363,
461-467

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 12-23

Carboxylesterases type-B serine active site.

amino acids 216-232

FIGURE 13

CATGGAGCCTCTTGCAGCTTACCCGCTAAAAATGTTCCGGGCCAGAGCAAAGGTATTTGCAG
 TTTTGCTGTCTATAGTTCTATGCACAGTAACGCTATTCTTCTACAACATAAAATTCCTCAAA
 CCTAAAAATCAACAGCTTTTATGCCTTTGAAGTGAAGGATGCAAAAGGAAGAACTGTTTCTCT
 GGAAAAGTATAAAGGCAAAAGTTTCTAGTTGTAAACGTGGCCAGTGACTGCCAACTCACAG
 ACAGAAATTACTTAGGGCTGAAGGAAGTGCACAAAGAGTTTGACCATCCCACTTCAGCGTG
 TTGGCTTTTCCCTGCAATCAGTTTGGAGAATCGGAGCCCCGCCCAAGCAAGGAAGTAGAATC
 TTTTGAAGAAAAAACTACGGAGTAACCTTTCCCATCTTCCACAAGATTAAGATTCTAGGAT
 CTGAAGGAGAACCTGCATTTAGATTTCTTGTGATTCTTCAAGAAGGAACCAAGGTGGAAT
 TTTTGAAGTATCTTGTCAACCTGAGGGTCAAGTTGTGAAGTCTGAGAGCCAGAGGAGCC
 CATTGAAGTCATCAGGCCTGACATAGCAGCTCTGGTTAGACAAGTGATCATAAAAAAGAAAG
 AGGATCTAT**TGA**GAATGCCATTGCGTTTCTAATAGAACAGAGAAATGTCTCCATGAGGGTTTG
 GTCTCATTTTAAACATTTTTTTTTTGGAGACAGTGTCTCACTCTGTCACCCAGGCTGGAGTG
 CAGTAGTGCCTTCTCAGCTCATTGCAACCTCTGCCTTTTTAAACATGCTATTAATGTGGCA
 ATGAAGGATTTTTTTTAAATGTTATCTTGCTATTAAAGTGGAATGAATGTTCCAGGATGAG
 GATGTTATCCCAAAGCAAAATCAAGAGTAGCCAAAGAATCAACATGAAATATATTAATACTACT
 TCCTCTGACCATACTAAAGAATTGAGAATACACAGTGACCAATGTGCCTCAATATCTTATTG
 TTCAACTTGACATTTTCTAGGACTGTACTTGATGAAATGCCAACACACTAGACCACTCTTT
 GGATTCAAGAGCACTGTGTATGACTGAAATTTCTGGAATAACTGTAAATGGTTATGTTAATG
 GAATAAAACACAAATGTTGAAAAATGAAAAATATATATACATAGATTCAAATCCTTATATAT
 GTATGCTTGTGTTGTACAGGATTTTGTGTTTTCTTTTTTAAGTACAGGTTCCCTAGTGTTTT
 ACTATAACTGTCACATATGTATGTAACAGACATATATAAATAGTCATTTATAAATGACCGTAT
 TATAACATTTGAAAAGTCTTCATCAAAAAAAAAAAAAAA

FIGURE 14

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA80136
><subunit 1 of 1, 209 aa, 1 stop
><MW: 23909, pI: 9.68, NX(S/T): 0
MEPLAAYPLKCSGPRAKVFAVLLSIVLCTVTLFLLQLKFLKPKINSEFYAFEVKDAKGRTVSL
EKYKGVSLVVNVASDCQLTDRNYLGLKELHKEFGPSHFVLAFFPCNQFGESEPRPSKEVES
FARKNYGVTFPIFHKIKILGSEGEPAFRFLVDSSKKEPRWNFWKYLVNPEGQVVVKFWRPEEP
IEVIRPDIAALVRQVIKKKEDL
```

Important features of the protein:

Signal peptide:

amino acids 1-31

Glutathione peroxidases signature 2.

amino acids 104-112

Glutathione peroxidases.

amino acids 57-82

FIGURE 15

TGTGCGCTGGCCCTCGCCATGCGAGACCCCGGAGCGTCCCTCCCGCGCGGCCCTCTGCTTCTGCTGTGCTA
 CTGGGGGGGCGCCACGGCCTCTTTCCTGAGGAGCGCGCGCGCTTAGCGTGGCCCCGAGGACCTACCTGAACCA
 CATCCCGCTGTTTGTGGGCAGCGGGCCCGAGCGCTGACCCCCGAGAAGGTCTGACGACTCAACAGCAGCA
 GTCTCGCGGGTCAACAGGAGCGGTGTTTCATTGGGGACAGGGACAACCTCTACCGCGTAGAGCTGGAGCCCCCAG
 TCCACGGAGTCCGGTACAGAGAGGAAGTGAACCTGGAGATCTAACCCACGACACATAAGCGTGTCTGGATGAG
 GGCAACAGGAGGGCGAGTGTGCAAACTTCGTAAGGTGTGCTCCTTCGGGACGAGTCCAGCGCTCTTTGTGTGG
 GGTTCACACGCTTCAACCCGGTGTGGCCAACTACAGCATAGACACCTTGACGCGCGTGGAGACAACATCAGC
 GGTATGGCGCGCTGCCGTACGACCCCAAGCAGCGCAATGTTGCCCTTCTCTGAGGGATGCTCTTACAGCT
 ACTGTTACGACTCTCTGACCATTTGATGCTGTATCTACCGAGCCTCGGGGACAGGCCACCTCGGCGACCGTG
 AAACATGAGTCCAACTGTTTCAAGAGCCTTACTTTGTCATGCGGTGGAGTGGGCGAGCATGTCTACTCTTTC
 TTCGGGAGATTGCGATGGAGTTTAACTACCTGGAGAAGGTGGTGGTGTCCCGCGTGGCCCGAGTGTGCAAGAAC
 GACGTGGGAGGCTCCCCCGCGTGTGGAGAAGCAGTGGACGTCTTCTCAAGGCGCGGCTCAACTGCTCTGTA
 CCGGAGACTCCCATTTCTACTTCAACGTGTGCAGGCTGTACGGGCGTGGTCAAGCTCGGGGGCGGGCCGTG
 GTCTTGCGCGTTTTCACGCCAGCAACAGCATCCCTGGCTCGGCTGTCTGCGCCTTTGACTGACACAGGTG
 GCAGCTGTGTTGAAGGCGGCTTCGAGAGCAGAAGTCCCGGAGTCCATCTGGACGCGGCTGCCGGAGGATCAG
 GTCCCTCGACCCCGGCCCGGTTGTCGCGAGCCCCGGGATGCAGTACATGCTCCAGCGCTTCCCGGATGAC
 ATCTCTCAACTTTGTCAAGACCCACCTCTGATGGACGAGGCGGTGCCCTCGTGGCCCTGCGCCCTGGATCTGT
 CGGACCTGATGAGGACCCAGCTGAGTGGCTGTGGAGCTGGGCGCGGCCCTCGGGCAACACAGGACCTGT
 GTCTTCTCGGTTCTTGGGCGGGGACGGTCTCAAGTTCCTGTGCGGCCAATGCCAGACCTCAGGACGCTGT
 GGGCTCAGTGTCTTCCGTGGAGGTTTGAACCTACCGGCCGAGACAGTGTGGAGCGCCCGCGGTTGGCGAGACA
 GGGCAGCGGCTGCTGAGCTTGGAGCTGGACGAGCTTCGGGGGCGCTGTGCTGCTCTCCCGCGTGGTGGTG
 CGAGTGTGCTGTGCTGCTGCCAGCACTACTCGGGGTGTATGAAGAATGTATCGGCACTCAGGACCCCTACTGC
 GGGTGGGCCCCGAGCGGCTCTGCATCTTCTCAGCCCCGGGACCAAGGCCCTTTGACGAGGAGGTGTGCCGGG
 CGCAGCACTCAGGCTTAGGGCTGCACAGGACTCTCGGGCGGCGAGTCTCGGAGGCGCGCGGGGCTGTGT
 TCGGTCAACTGCTGCTGAAGTCTCTCGTGGCGGCTCTCGTGGTGGGAGCGCTGGTGTCTCGGCTTCAGCTGGG
 TGGTTCTTGGGCTCCGTGAGCGCGGAGCTGGCCCGCGCGCAAGGACAGGCACTCTGGCGACCGGGCTGTGT
 TCGGTGAGCTGCTGCTGAGCTACCGGCTGGGCGAGCGCAGGGCGAGGCTCCGGGCGCGGGCGAGGCGGT
 GCGGTTGGCGCGGCGCTCCCGGAGGCCCTGCTGGCGGCTGTGATGCAAGACGCTGGGCCAAGGCCACGCTG
 CTGAGGCGGGGCCACGACTGGACTCGGCTGCTGCCACGCCGAGCAGACGCGCTGCCGAGAGCGC
 CTGGCCACTCCGACCCGACCCACCGGCTGGGCCCCCGCGCTGGGACACAGGCCACCCCTGCTCCCGCG
 TCCGCTTCACTCTCTCTCTGTGTGGCGCCGCGCCGGGCCCGAGCAGCCCGCGCTGGGAGCGGAC
 CCGGAGCGGCGCTCTATGCTGCCGCGCGCGCGCGCGCTCCACGCGCACTTCCCGCTCACCCCCACGCGCAG
 CGGACCGCGCGGGGTGTGTCCGCGCCACGCGGCCCTTGGACCCAGCTCAGCGCGCGATGGCTTCCGCGG
 CCTGTGAGCGCGCGCCGACGGGACGCTGAGGAGGCCACTGGGCCCCACGCGCCTCGCGCGCCACCTGTGCG
 CGCACCAACAGCTTCAACAGCGCGGAGGCCCGGCTGGGGACCGCCACCGGCTGCCACGCGCGCGGGGACA
 GACTTGGCCACCTCTCTCCCTATGCGGGGCGGACAGGACTGCGCCCGCGTGGCCCTAGCGCGGGGGCGCCCG
 ATGCTTGGCAGTGGCCAGCCAGGGAACAGGAGCAGAGACGTTGCCAGAAGCGCGGGGCCCGGGGCACTCCG
 AGTGGGTGCTCAAGTCCCCCGCGACCCACCGCGAGTGGGGGCGCCCTTCGCGCACAGGAAGCACAACAG
 TCTGCCCTTCCCTACCCGGGCGCGAGGACGCTGAGACGTTTGGGGGTGGGTGGCGGGAGGACTTTCATG
 GATTGTAGGTTGACCTTATGCGCGTAGGTTTGGTTTTTTTTTCGAGTTTGGTTTCTTTTTCGCTTTTCAACC
 AATTGACCAACTCCCTTCTCGGGTGGCGGAGCGAGCGAGGCTTGGACGCGGTGGGGAATTGGGGGGCCAG
 CTGACAGACTAAGCCCTCCCCACCCCTGGAAGGTCCTTCCCAACCCAGGCCCTGGGCTGTGTGGGTGTGCG
 TGCGTGTGCGTGCTGTGTTGCTGTGCAAGGGCGGGGAGGTGGCGTGTGTGTGCTGTCACGCAAGGTGTGCG
 TGGCGGTGTGTGTCAAGTGGGCGAGCGGTGAGGTTGTGTTCACAGCGCAGCATGTTGGTGGCCCGAGGGCC
 TGGGCTTGGCTGGGCGTGGGCTGGGCTTCCAGAAGCGCGGGCTCCTCGAGTGGCGGTTAGGAGTTTGAAC
 CCCCCCACTCTGACAGGGAAGCGGGGACAAATGCCGGGTTTCAGGACGAGACAGGAGGGGCTTGGCCGA
 AGTCACTGAGCAGGAGTGTCTAAAGGCTTGGGGCTGGGGGCGCGGAGGTGGGCGCCCTCTGTAA
 ATACGGCCCCAGGTTGGTGAAGAGTCCATGCCACCGCTCCCTTGTGACTCCCCCTATGACTCCAGCTGA
 CCATGCGTCCAGCTGGCTGCTGCTGGTCTCTGCGCTCTTGGAGTTTGGCTCCCGCGCCCTCCCATCAAT
 AAAACTCTGTTTACAAACAAAAAATAAAAAAAAAAAAAAAAAA

FIGURE 16

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA80145

><subunit 1 of 1, 888 aa, 1 stop

><MW: 95285, pI: 8.89, NX(S/T): 8

MQTPRASPPRALLLLLLLGGAGHLFEEPPPLSVAPRDYLNHYPVFVSGSPGRLTPAEGA
DDLNIIQVRLVRNRTLFIGDRDNLVRVELEPPTSTELRYQRKLTWRSNPSDINVCRMKGQEG
ECRNFKVLLLRDESTLFVCGSNAFNPVCANYSIDTLQPVGDNISGMARCPYDPKHAVALF
SDGMLFTATVTDFLAIDAVIYRSLGDRPTLRTVKHDSKWFKEPYFVHAVEWGSHVYFFFREI
AMEFNYLEKVVVSRVARVCKNDVGGSPRVLEKQWTSFLKARLNCSVPGDSHFYFNVLQAVTG
VVSLGGRPVVLAVFSTPSNSIPGSAVCAFDLTQVAAVFEGRFREQKSPESIWTVPVEDQVPR
PRPGCCAAPGMQYNASSALPDDILNFVKTHPLMDEAVPSLGHAPWILRTLMRHQLTRVADV
GAGPWGNQTVVFLGSEAGTVLKFVLRPNASTSGTSGLSVFLFEEFETYRPDRCGRPGGGGTGQ
RLLSLELDAASGGLLAAPRCVVRVPVARCQYSGCMKNCIGSDPYCGWAPDGSCI FLSPG
TRAAFEQDVSGASTSGLGDCTGLLRASLSEDRAGLVSVNLLVTSSVAAFVVGAVVSGFSVGW
FVGLRERRELARRKDKKAILAHGAGEAVLSVSRLGERRAQPGGGRGGGGGGGAGVPPEALLA
PLMQNGWAKATLLQGGPHLDLSGLLPTPEQTPLPQKRLPTPHPHPHALGPRAWDHGHPLPA
SASSSLLLLAPARAPEQPPAPGEPTPDGRLYAARPGRASHGDFPLTPHASPDORRRVVSAPTG
PLDPASAADGLPRPWSPPPTGSLRRPLGPHAPPAATLRRTHTFNSGEARPGDRHRGCHARPG
TDLAHLPLPYGGADRTAPPVF

Important features of the protein:

Signal peptide:

amino acids 1-25

Transmembrane domains:

amino acids 318-339, 598-617

N-glycosylation sites.

amino acids 74-78, 155-159, 167-171, 291-295, 386-390, 441-445,
462-466

Glycosaminoglycan attachment sites.

amino acids 51-55, 573-577

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation sites.

amino acids 21-27, 50-56, 189-195, 333-339, 382-388, 448-454,
490-496, 491-497, 508-514, 509-515, 531-537, 558-564, 569-575,
574-580, 580-586, 610-616, 643-649, 663-669, 666-672, 667-673,
668-674, 669-675, 670-676, 868-874, 879-885

FIGURE 17

AGCAACTCAAGTTCATCATTGTCTGAGAGAGAGGAGCAGCGCGGTTCCTCGGCCGGGACAGC
 AGAAGCGCCAGGGGACCCTCACCTGGGCGCGCCGGGGCACGGGCTTTGATTGTCTTGGGTCG
 CGGAGACCCGCGCGCCTGCCCTGCACGCCGGGGCGGAACCTTTGCAGTCGCTTGGCTGCTG
 CGATCGGCCGCGGGTCCCTGCCGAAGGCTCGGCTGCTTCTGTCCACCTCTTACACTTCTTC
 ATTTATCGGTGGATCATTTCGAGAGTCCGTCTTGTAATGTTTGGCACTTTGGCTACTTTATT
 GCTTCTTTCTGGCGACAGTTCAGCACTCGCCGAGACCGGCGGAGAAAGGCAGCTGAGCCCG
 GAGAAGAGCGAAATATGGGGACCCGGGCTAAAAGCAGACGTGCTCCTTCCCGCCCGTATTT
 CTATATTCAGGCAGTGGATACATCAGGGAATAAATTCACATCTTCTCCAGGCGAAAAGGTCT
 TCCAGGTGAAAGTCTCAGACCAGAGGAGCAATTCACTAGAGTTGGAGTCCAGGTTTTAGAC
 CGAAAAGATGGTCTTCTATAGTAAGATACAGAATGTATGCAAGCTACAAAAATCTGAAGGT
 GGAAATTAATTCGAAGGCAACATGTGCCAAATCCCATATATTTTAAAGGGCCGTTT
 ACCATGAGAACTGTGACTGTCTCTGCAAGATAGTGACCGTGGCTACGGGAGATGAAGTGC
 CCTGAAACCATTGCTCAGATTCAAGAGATCTGGCAGATTTCCCTGCTGTGGATCCAGAAAA
 GATTGCAAGTAAATCCCAAAAGATTGGACAGAGGCAGAGCCTATGCTACTACACCTTAA
 AGGATAACAAGGTTTATATCAAGACTCATGGTGAACATGTAGGTTTTAGAATTTTATGGAT
 GCCATACTACTTTCTTTGACTAGAAAGGTGAAGATGCCAGATGTGGAGCTCTTTGTTAATTT
 GGGAGACTGGCCTTTGGAAAAAAGAAATCCAATTCAAACATCCATCCGATCTTTTCTGGT
 GTGGCTCCACAGATTCCAAGGATATCGTGATGCCTACGTACGATTTGACTGATTCGTCTTG
 GAAACCATGGGCCGGGTAAGTCTGGATATGATGTCGTCGCAAGCTAACACGGGTCCTCCCTG
 GGAAAGCAAAAATCCACTGCCGTCTGGAGAGGGCGAGACGCCGCAAGAGAGACTCGAGC
 TGGTTAAACTCAGTAGAAAAACCCAGAACTCATAGACGCTGCTTACCAACTTTTTCTTC
 TTTAAACACGATGAAAACCTGTATGGTCCCATTTGTGAAACATATTTTCATTTTTTGATTTCTT
 CAAGCATAAGTATCAATAAATATCGATGGCACTGTAGCAGCTTATCGCCTGCCATATTTGC
 TAGTTGGTGACAGTGTGTGCTGAAGCAGGATTCCATCTACTATGAACATTTTTACAATGAG
 CTGCAGCCCTGGAAACACTACATTCCAGTTAAGAGCAACCTGAGCGATCTGCTAGAAAACT
 TAAATGGGCGAAAGATCACGATGAAGAGGCCAAAAAGATAGCAAAAGCAGGACAAGAATTTG
 CAAGAAATAATCTCATGGGCGATGACATATTCTGTTATTATTTCAAACCTTTTCCAGGAATAT
 GCCAATTTACAAGTGAAGTGAAGCCCAATCCGAGAGGGCATGAAAAGGTTAGAACCACAGAC
 TGAGGACGACCTCTTCCCTTGTACTTGCCATAGGAAAAAGACCAAGATGAAGTCTGATATG
 CAAAATAACTTCTATTAGATAATGGTGCTCTGAAGACTCTTCTTAACATAAAAGAGAAATT
 TTTTAAAGTATTAATCCATGGACAATATAAAATCTGTGTGATTGTTTGCAGTATGAAGACA
 CATTTCTACTTATGCAGTATTCTCATGACTGTACTTTAAAGTACATTTTTAGAATTTTATAA
 TAAACCACCTTTATTTTAAAGGAAAAAA

FIGURE 18

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA84917
><subunit 1 of 1, 502 aa, 1 stop
><MW: 58043, pI: 7.94, NX(S/T): 2
MFGTLLLYCFFLATVPALAEETGGERQLSPEKSEIWGPGLKADVLPARYFYIQAVDTSGNKF
TSSPGKEKVFQVKVSAPEEQFTRVGVQVLD RKDGSFIVRYRMYASYKNLKV EIKFQGQHVAKS
PYILKG PVYHENCDCPLQD SAAWLREMNC PETIAQIQ RDLAHFPAVDPEKIAVEIPKRFGQR
QSLCHYTLKDNKVYIKTHGEHVGFRI FMDAILLSL TRKVKMPDVELFVN LGDWPLEKKKSNS
NIHPIFSCWGSTD SKDIVMPTYDLTDSVLETMGRVSLDMMSVQANTGPPWESKNSTAVWRGR
DSRKERLELVKLSRKHP ELIDAAFTNFFFFKH DENLYGPIVKHISFFDFFKH KYQINIDGTV
AAYRLPYLLVGDSVVLKQDSIYYEHFYNELQPWKHYIPVKS NLSDLLEK LKWAKDHDEEAKK
IAKAGQEFARNNLMGDDIFCYYFKLFQ EYANLQVSEPQIREGMKRVEPQTEDDLFPCTCHRK
KTKDEL

Important features of the protein:

Signal peptide:

amino acids 1-17

N-glycosylation sites.

amino acids 302-306, 414-418

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 243-247, 495-499

Tyrosine kinase phosphorylation site.

amino acids 341-348

N-myristoylation sites.

amino acids 59-65, 118-124, 184-190, 258-264, 370-376, 439-445

Endoplasmic reticulum targeting sequence.

amino acids 499-504

FIGURE 19

CCTGGAGCCGGAAGCGCGGCTGCAGCAGGGCGAGGCTCCAGGTGGGGTCGGTTCGCGATCCA
 GCCTAGCGTGTCACCAATGCGGGTGGGCTCCGGGACTTTTCGCTACCTGTTGCGTAGCGATCG
 AGGTGCTAGGGATCGCGGTCTTCTTCGGGGATTCTTCCCGGCTCCCGTTCGTTCTCTCTGCC
 AGAGCGGAACACGGAGCGGAGCCCCAGCGCCCGAACCTTCGGCTGGAGCCAGTTCTAACTG
 GACCACGCTGCCACCACCTCTCTTCAGTAAAGTTGTTATTGTTCTGATAGATGCCCTTGAGAG
 ATGATTTTGTGTTTGGGTCAAAGGGTGTGAATTTATGCCCTACACAACCTACCTTGTGGAA
 AAAGGAGCATCTCACAGTTTGTGGCTGAAGCAAAGCCACCTACAGTTACTATGCTCGAAT
 CAAGGCATTGATGACGGGGAGCCTTCTGGCTTTGTCGACGTCATCAGGAACCTCAATTCTC
 CTGCACTGCTGGGAAGACAGTGTGATAAGACAGCAAAAGCAGCTGGAAGAAAGAAATAGTCTTT
 TATGGAGATGAAACCTGGGTAAATTATTCCTAAAGCATTGTTGGAATATGATGGAACAC
 CTCATTTTTCGTGTGATGATTACACAGAGGTGGATAATAATGTACAGAGGCATTGATGATAAAG
 TATTAAGAGGAGATTGGGACATATTAATCTCCACTACCTGGGCTGGACCACATTGGC
 CACATTTTCAGGGCCCAACAGCCCCCTGATTGGGCAGAAAGCTGAGCGAGATGGACAGCGTCT
 GATGAAGATCCACACCTCACTGCAGTCGAAGGAGAGAGAGACGCCCTTACCCAATTTGCTGG
 TTTCTTTGTGGTGACCATGTCTGAAACAGGAAGTCACGGGGCCTCTCCACCGAGGAG
 GTGAATACACCTCTGATTTTAAATCAGTTCTGCGTTTGAAGGAAACCCGGTGATATCCGACA
 TCCAAAGCACGTCCTAATAGACGGATGTGGCTGCGACACTGGCGATAGCACTTGGCTTACCGA
 TTCCAAAGACAGTGTAGGGAGCCTCTATTCCAGTTGTGGAAGGAAGACCAATGAGAGAG
 CAGTTGAGATTTTACATTTGAATACAGTGCAGCTTAGTAAACTGTTGCAAGAGAATGTGCC
 CTCATATGAAAAGATCCTGGGTTTGAGCAGTTTAAATGTGAGAAAGATTGCATGGGAAC
 GGATCAGACTGTACTTGGAGGAAAAGCATTGAGAAGTCCATTCAACCTGGGCTCCAAGGTT
 CTCAGGCAGTACCTGGATGCTCTGAAGACGCTGAGGTTGTCCCTGAGTGCACAAGTGGCCCA
 GTTCTCACCCCTGCTCTGCTCAGCGTCCACAGGCAGTGCACAGAAAGGCTGAGCTGGAAGT
 CCCACTGTCATCTCTGGGTTTTCTCTGCTCTTTATTGTTGATCCTGGTCTTTTCGGCCG
 TTCACGTCATTGTGTGCACCTCAGCTGAAAGTTTCGTGCTACTTCTGTGGCCTCTCGTGGCTG
 GCGGCAGGCTGCCTTTGTTTACCAGACTCTGGTTGAACACCTGGTGTGTGCCAAGTGCTGG
 CAGTGCCCTTGACAGGGGGCTCAGGGAAGGACGTTGAGCAGCCTTATCCCAGGCCCTCTGGG
 TGTCGCCACACAGGTGTTACATCTGTGCTGTGCTCAGGTGAGTGCCTCAGTTCTTGAAAGCT
 AGGTTCTCGGACTGTTACCAAGGTGATTGTAAAGAGCTGGCGGTACAGAGGAACAAGCCC
 CCCAGCTGAGGGGGTGTGTGAATCGGACAGCCTCCAGCAGAGGTGTGGGAGCTGCAGCTGA
 GGAAGAAGAGACAATCGGCCCTGGACACTCAGGAGGGTCAAAGGAGACTTGGTGCACACAC
 TCATCTGCCACCCCCAGAAATGCATCTGCCTCATCAGGTCCAGATTTCTTTTCAAGCGGA
 CGTTTTCTGTTGGAATTTAGTCTTGGCCTCGGACACCTTCAATTCGTTAGCTGGGGAGTG
 GTGGTAGGACAGTGAAGAAGGCGGATGGTCACACTCAGATCACAGAGCCAGGATCAAG
 GGACCCACTCAGTGGCAGCAGGACTGTTGGGCCCCACCCCAACCTGTCACAGCCCTCATC
 CCCTCTTGGCTTGAGCCGTGAGGGCCTGTGCTGAGTGTCTGACCCAGACACTCAGCTT
 GTGCATCAGGGCACAGGCTTCTCGGAGCCAGGATGATCTGTGCCACGCTTGCACCTCGGGC
 CCATCTGGGCTCATGCTCTCTCTGCTATTGAATTAGTACCTAGCTGCACACAGTATGTA
 GTTACCAAAAGAATAAACGGCAATAATTGAGAAAAAAA

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FIGURE 21

AGCCAGGCAGCACATCACAGCGGGAGGAGCTGTCCCAGGTGGCCAGCTCAGCAATGCAAT
 GGGGGTCCCCAGAGTCATTCTGCTCTGCCTCTTTGGGGCTGCGCTCTGCCTGACAGGGTCCC
 AAGCCCTGCAGTGCTACAGCTTTGAGCACACCTACTTTGGCCCTTTGACCTCAGGGCCATG
 AAGCTGCCCAGCATCTCCTGTCTCATGAGTGCTTTGAGGCTATCCTGTCTCTGGACACGG
 GTATCGCGCGCCGGTGACCCTGGTGCGGAAGGGCTGCTGGACCGGGCCCTCCTGCGGGCCAGA
 CGCAATCGAACCCGGACGCGCTGCCGCCAGACTACTCGGTGGTGCGCGGCTGCACAACTGAC
 AAATGCAACGCCACCTCATGACTCATGACGCCCTCCCCAACCTGAGCCAAGCACCCGACCC
 GCCGACGCTCAGCGGCGCCGAGTGCTACGCCTGTATCGGGGTCCACCAGGATGACTGCGCTA
 TCGGCAGGTCCCGACGAGTCCAGTGTCACCAGGACCAGACCGCCTGCTTCCAGGGCAGTGGC
 AGAATGACAGTTGGCAATTTCTCAGTCCCTGTGTACATCAGAACCTGCCACCGGCCCTCCTG
 CACCACCGAGGGCACCACCAGCCCCGGACAGCCATCGACCTCCAGGGCTCCTGCTGTGAGG
 GGTACCTCTGCAACAGGAAATCCATGACCCAGCCCTTACCAGTGCTTCAGCCACCACCCCT
 CCCCAGCACTACAGGTCTTGGCCCTGCTCCTCCAGTCTCTCTGCTGGTGGGGCTCTCAGC
 ATAGACCGCCCTCCAGGATGCTGGGGACAGGGCTCACACACCTCATTCCTTGTGCTTCAGC
 CCCTATCACATAGCTCACTGGAATGATGTTAAAGTAAGAATTGCAAAA

FIGURE 22

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA86576

><subunit 1 of 1, 251 aa, 1 stop

><MW: 26935, pI: 7.42, NX(S/T): 2

MAMGVPRVILLCLFGAALCLTGSQALQCYSFEHTYFGPFDLRAMKLPSISCPHECFEAILSL
DTGYRAPVTLLVRKGCWTGPPAGQTQSNPDALPPDYSVVRGCTTDKCNALMTHDALPNLSQA
PDPPTLSGAECYACIGVHQDDCAIGRSRRVQCHQDQTACFQGSGRMTVGNFSPVYVIRTCHR
PSCTTEGTTSPWTAIDLQGSCEGYLCNRKSMTQPFTSASATTPPRALQVLALLLPVLLLVGLSA

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 233-251

N-glycosylation sites.

amino acids 120-124, 174-178

N-myristoylation sites.

amino acids 15-21, 84-90

FIGURE 23

CCCACGCGTCCGGGACAGATGAACCTAAAAGAGAAGCTTTAGCTGCCAAAGATTGGGAAAGG
 GAAAGGACAAAAAGACCCCTGGGCTACACGGCGTAGGTGCAGGGTTTCTACTGCTGTCT
 TTTATGCTGGGAGCTGTGCTGTAAACCAACTAGGAAATAACGTATGCAGCAGCTATGCGGTGT
 CAGAGAGTTGTGCTTCCCAAGACAAAGGCAAGTCTCTTTCTTTTCTTTTGGGAGTGT
 CCTTGGCAGGTTCTGGGTTTGGACGTTATTCCGGTACTGAGGAAACAGAAAAGGATCCTTT
 GTGGTCAATCTGGCAAAAGGATCTGGGACTAGCAGAGGGGGAGGTGGCTGCAAGGGGAAACCA
 GGTGGTTTCCGATGATAACAACAATACTCTGCTCTGGATTACATACCCGGAAATTGCTCA
 CAAATGAGAACTGGACCGAGAGAAGCTGTGTGGCCCTAAAGAGCCCTGTATGCTGTATTTT
 CAAATTTTAAATGGATGATCCCTTTCAGATTACCGGGCTGAGGTGAGAGTCAGGGATATAAA
 TGATCACGCGCCAGTATTTTCAGGACAAAGAAACAGTCTTAAAAATATCAGAAAAACAGCTG
 AAGGGACAGCATTTAGACTAGAAAGAGCACAGGATCCAGATGGAGGACTTAACGGTATCCAA
 AACTACACGATCAGCCCAACTCTTTTTCATATTAACTATTAGTGGCGGTGATGAAGCAT
 GATATATCCAGAGCTAGTGTGGACAAAGCACTGGATCGGGAGGAGCAGGGAGAGCTCAGCT
 TAACCTTCCACAGCGCTGAATGGTGGGTCTCCATCCAGGTCTGGGACCTCTACTGTACGCATC
 GTTGCTTGGACGTCGATTGACAATGCCACAGTTTGCCACAGCTCTGTATGAGACCGAGGC
 TCCAGAAAAACAGCCCATTTGGGTCTCTTATTGTTAAGGTATGGGCAGAAAGATGTAGACTCTG
 GAGTCAACGCGGAAGTATCTTATTCATTTTGTATGCTCAGAAAAATATTCGAACGACCTTT
 CAAATCAATCCTTTTTCTGGGAAATCTTTCTCAGAGAATTGCTTGATTATGAGTTAGTAAA
 TTCTTACAAAATAAATATACAGGCAATGGACGGTGGAGGCCCTTTCTGCAAGATGTAGGGTTT
 TAGTGAAAGTATTGGACCAATGACAATCCCCCTGAACGTATCATCATTTTCCAAC
 TCTGTTGCTGAGAATTCTCCTGAGACGCCGCTGGCTGTTTTTAAGATTAAATCAGACAGACTC
 TGGAGAAAAATGGAAAGATGGTTTGTCTACATTCAGAGAATCTGCCATTCCTACTAAAACCTT
 CTGTGGAGAAATTTTACATCTTAATTACAGAGGGCGCGCTGGACAGAGAGATCAGAGCGAG
 TACAACATCTACTATCACCGTCACTGACTTGGGGACACCCAGGCTGAAAAACCGAGCACAACT
 AACGGTCTCTGCTCCGACGTCAATGACAACGCCCGCCGCTCTCACCCAAACCTCTACACCC
 TGTTCGTCCGCGAGAACACACAGCCCGCCCTGCACATCCGACGCTACAGCGCCACAGAGA
 GACTCGGGGCAACCAACGCCACGGTCACTACTCGTGTCTGCCGCCCAAGACGCCCACTGCC
 CCTCGCTCCCTGGTCTCCATCAACGCGGACAAACGGCCACCTGTTCGCCCTCAGGTGCTGG
 ACTACGAGGCCCTGCAGGCTTTCGAGTTCGCGCTGGGCGCCACAGACCGCGGCTCCCCGCG
 CTGAGCAGAGAGGCGCTGGTGCAGCTGCTGGTGTGGACGCAACAGCAACTCGCCCTTCGT
 GCTGTACCCGCTGCAGAACGGCTCCGCGCCCTGCACCGAGCTGGTGCCCGGGCGGCCGAGC
 CGGGCTACCTGGTGACCAAGGTGGTGGCGGTGGACGGGACTCGGGCCAGAACGCTGGCTG
 TCGTACCAGCTGCTCAAGGCCACGGAGCCCGGGCTGTTCCGTGTGTGGGCGCACATGGGGA
 GGTGCGCACCGCCAGGCTGCTGAGCGAGCGCGACGCAAGCAAGCAGCTCGTGGTGTCTTG
 TCAAGGACAAATGGCGAGCTCTCTCGCTCGGCCACCGCCACGCTGCATCTGCTCTGGTGAC
 GGGTTCTCCAGCCCTACCTGCCCTCTCCGAGGGCGGCCCGGCCAGGCGCCAGGCGGAGGC
 CGACTTGCTCACCGTCTACCTGGTGGTGGCGTGGCCCTCGGTGTCTTCGCTCTCTCTCTCT
 CGGTGCTCTGTGCTGGCGGTGCGGCTGTGCGAGGAGGAGCAGGGCGGCCCTGGTGGGTGCG
 TGCTCGGTGCCGAGGGTCTTTTCCAGGGCATCTGGTGGACCTGAGGGGCGCTGAGACCTT
 GTCCAGAGCTACCGATATGAGGTGTGTCTGACGGGAGGCCCGGGGACCACTGAGTTCAAGT
 TCTTGAACCACTGTTATTCGATATTGAGGCACAGGGCCCTGGGAGGAAAGGTGAAGAAAAAT
 TCCAGCTTCCGAAATAGCTTTGGATTAAATATTCAGTAAAGTCTGTTTATGTTCTATATAC
 TTTTGGTGTGTACATAGCCATGTTTCTATTAGTTTACTTTTAACTCTCAAAATTTAAGTAT
 TATGCAACTTCAAGAAATTTTCAAGTAGTATACCCCTGTGGTTTTCAAGTGTTCATCAT
 TTTTTGCTATTAATAAACAACCTGGGTTTAATTTAATGAGTATTTTTTCTAAATGATAGTGT
 AAGGTTTTAATCTTTTCCAACCTGCCAAGGAATTAATTAATATATATCTCATTTACAGAAAT
 CTGAGGTTTTGATTCTTTTCAGAGCTTCATCTCATGATCTAATCACTCTGCTATAGTG
 TACTTGCTCTATTTAAGAAGGCATATACATTTCCAAACTCATTTCAACATCTATATAT
 CGTGTGTGAAAAACCATGTCATTTATTCTACATCATGTATTTAAAAAGAAATTTTCTCTAC
 TACTATGCTCATGACAAATGAACAAAGCATATTGTGAGCAATACTGAACTCAATCAATAATAC
 CCTTAGTTTATATACTATATATTTATCTTTAAGCATGCTACTTTTACTTGGCCAAATATTT
 CTTATGTTAACTTTTGTGATGATAAAACAGACTATGCTCTATAATGAATAAAATTATA
 ATCTGCTGAAAAATGAATAAAAAATAAACATTTTGAATGTGAAAAAAAAAAAAAAAAAAAA

FIGURE 24

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA87976

><subunit 1 of 1, 800 aa, 1 stop

><MW: 87621, pI: 4.77, NX(S/T): 7

MAVRELCPFRQRVLFLEFLFWGVSLAGSGFGGRYSVTEETKSGSFVVNLAKDLGLAEGELAAAR
GTRVVSDDNKQYLLLDSTGNLLTNEKLDREKLCGPKEPCMLYFQIIMDDPFQIYRAELRVR
DINDHAPVFQDKETVLKISENTAEGTAFRLERAQDPDGGGLNGIQNYTISPNSFFHHINISGGD
EGMIYPPELVLDKALDREEQGELSLTLTALDGGSPSRSGTSTVRIVVLVDNDNAPQFAQALYE
TQAPENSPIGFLIVKVAEDVDSGVNAEVSYSFFDASENIRTTFFQINPFSGEIFLRELLDYE
LVNSYKINIQAMDGGGLSARCRVLVEVLDTNDNPPELIVSSFSNSVAENSPETPLAVFKIND
RDSGGENGMVCYIQENLPFLKPSVENFYILITEGALDREIRAEYNITITVDTLGTPLRKTE
HNITVLVSDVNDNAPAFQTSTYTLFVRENNSPALHIGSVSATDRDSTGNAQVTSYLLPPQDP
HLPLASLVSLINADNGHLFALRSLDYEALQAFEFVRGATDRGSPALSREALVRVLVDANDNS
PFVLYPLQNGSAPCTELVPRAAEPGYLVTKVVAVDGDGSGQNAWLSYQLLKATEPGLFGVWAH
NGEVRTARLLSERDAAKHRLVVLVKDNGEPPRSATATLHLLLVLDGFGSQPYLPLPEAAPAQAO
AEADLLTVYLVVALASVSSLFLLSVLLFVAVRLCRRSRAASVGRCSVPEGFPFPHLVDVRGA
ETLSQSYQYEVCLTGGPGTSEFKFLKPVISDIQAGGPGRKGEENSTFRNSFGFNIQ

Important features of the protein:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 687-711

N-glycosylation sites.

amino acids 169-173, 181-185, 418-422, 436-440, 567-571, 788-792

Glycosaminoglycan attachment site.

amino acids 28-32

Tyrosine kinase phosphorylation sites.

amino acids 394-402, 578-585

N-myristoylation sites.

amino acids 22-28, 27-33, 53-59, 82-88, 162-168, 184-190,
217-223, 324-330, 325-331, 471-477, 568-574, 759-765

Amidation site.

amino acids 781-785

Aminoacyl-transfer RNA synthetases class-II signature 1.

amino acids 117-138

Cadherins extracellular repeated domain signature.

amino acids 121-132, 230-241, 335-346, 439-450, 549-560

FIGURE 25

GAATGAATACCTCCGAAGCCGCTTTGTTCTCCAGATGTGAATAGCTCCACTATACCAGCCTC
GTCCTTCCTCCGGGGGACAACTGGGTCAGGGCACAGAGAGATATTTAATGTCACCCCTTGG
GGGCTTTCATGGACTCCCTCTGCCACATTTTTTGGAGGTTGGGAAAGTTGCTAGAGGCTTC
AGAACTCCAGCCTAATGGATCCCAACTCGGGAGAATGGCTCGCTCCCTGCTGGCTGTGCTG
CTGCTGCTGCTGGAGCGCGGCATGTTCTCCTCACCCCTCCCCGGCCGCGCTGTTAGAGAA
AGTCTTCCAGTACATTGACCTCCATCAGGATGAATTTGTGCAGACGCTGAAGGAGTGGGTGG
CCATCGAGAGCGACTCTGTCCAGCCTGTGCCTCGCTTCAGACAAAGAGCTCTTCAGAATGATG
GCCGTGGCTGCGGACACGCTGCAGCGCCTGGGGGCCGTGTGGCCTCGGTGGACATGGGTCC
TCAGCAGCTGCCCGATGGTCAGAGTCTTCCAATACCTCCCGTCATCCTGGCCGAACCTGGGGA
CGGATCCACGAAAGGCACCGTGTGCTTCTACGGCCACTTGGAGCTGCAGCCTGCTGACCGG
GGCGATGGGTGGCTCACGGACCCCTATGTGCTGACGGAGGTAGACGGGAACTTTATGGACG
AGGAGCGACCGACAACAAAGGCCTGTCTTGGCTTGGATCAATGCTGTGAGCGCCTTCAGAG
CCCTGGAGCAAGATCTTCTGTGAATATCAAATTCATCATTGAGGGGATGGAAGAGGCTGGC
TCTGTTGCCCTGGAGGAACCTGTGGAAGAAAGAAAGGACCGATCTTCTCTGGTGTGGACTA
CATTGTAATTTTCAGATAAAGCTGTGGATCAGCCAAAGGAAGCCAGCAATCACTTATGGAACCC
GGGGGAACAGCTACTTCATGGTGGAGGTGAAATGCAGAGACCAGGATTTTCACTCAGGAACC
TTTGGTGGCATCCTTCATGAACCAATGGCTGATCTGGTTGCTCTTCTCGGTAGCCTGGTGA
CTCGTCTGGTCATATCCTGGTCCCTGGAATCTATGATGAAGTGGTTCCCTTACAGAAGAGG
AAATAAATACATACAAGCCATCCATCTAGACCTAGAAGAAATACCGGAATAGCAGCCGGGT
GAGAAATTTCTGTTTCGATACTAAGGAGGAGATTCTAATGCACCTCTGGAGGTACCCATCTCT
TTCTATTTCATGGGATCAGGGGCGGTTTGGATGAGCCTGGAACTAAAAACAGTCATACCTGGCC
GAGTTATAGGAAAATTTTCAATCCGTCTAGTCCCTCACATGAATGTGTCTGCGGTGGAAGAAA
CAGGTGACACGACATCTTGAAGATGTGTTCTCCAAAAGAAATAGTTCCAAACAAGATGGTTGT
TTCCATGACTCTAGGACTACACCGTGGATTGCAAAATATTGATGACACCCAGTATCTCGCAG
CAAAAAGAGCGATCAGAACAGTGTGGAACAGAACAGATATGATCCGGGATGGATCCACC
ATTCCAATTGCCAAAATGTTCCAGGAGATCGTCCACAAGAGCGTGGTGCTAATTCGGCTGGG
AGCTGTTGATGATGGAGAACATTTCGAGAAATGAGAAAATCAACAGGTGGAATACATAGAGG
GAACCAATATTGCTGCCTTTTTCTTAGAGATGGCCAGCTCCATTAAACACAAAGAACCT
TCTAGTCTGATCTGATCCACTGACAGATTCACTCCCCACATCCCTAGACAGGGATGGAAT
GTAAATATCCAGAGAATTTGGGTCTAGTATAGTACATTTTCCCTTCCATTTAAAAATGTCTTG
GGATATCTGGATCAGTAATAAAATATTTCAAAGGCACAGATGTTGGAATGGTTTAAAGTCC
CCCACTGCACACCTTCTCAAGTCATAGCTGCTTGACGCAACTTGATTTCCTCAAGTCTGTG
GCAATAGCCCCAGGATTTGATTCTTCCAACCTTTTAGCATATCTCCAACCTTGAATTTGA
TTGGCATAATCACTCCGGTTTGCTTTTCTAGGTCTCAAGTGCTCGTGACACATAATCAATCC
ATCCAATGATGCGCTTTGCTTTACCACTCTTTCCTTTTATCTTATTAATAAAAATGTGGTCT
TCCACCACTGNCCTCCAAAAAAGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAA

FIGURE 26

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92234
><subunit 1 of 1, 507 aa, 1 stop
><MW: 56692, pI: 5.22, NX(S/T): 3
MDPKLGRMAASLLAVLLLLLLERGMFSSPPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESD
SVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAEIGSDPTK
GTVCFYGHLDVQPADRGDGLWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQD
LPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSY
FMVEVKCRDQDFHSGTGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTY
KAHLDLEEYRNSRVEKFLFDTKKEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGK
FSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMTLGLHPWIANIDDTQYLAAKRAI
RTVFGTEPDMIRDGSTIPIAKMFQEI VHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTLKF
AAFFLEMAQLH

Important features of the protein:

Signal peptide:

amino acids 1-26

Transmembrane domain:

273-292

N-glycosylation sites.

amino acids 322-326, 382-386, 402-406

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 400-404

N-myristoylation sites.

amino acids 89-95, 119-125, 162-168, 197-203, 242-248, 263-269,
351-357

Cell attachment sequence.

amino acids 140-143

ArgE / dapE / ACY1 / CPG:

amino acids 156-167

FIGURE 27

CTCGGCTGGATTAAAGGTTGCCGCTAGCCGCTGGGAATTTAAGGGACCCACACTACCTTCC
CGAAGTTGAAGGCAAGCGGTGATTGTTTGTAGACGGCGCTTTGTCA**ATG**GGACCTGTGCGGTT
GGGAATATTGCTTTTCTCTTTTTTTGGCCGTGCACGAGGCTTGGGCTGGGATGTTGAAGGAGG
AGGACGATGACACAGAACGCTTGCCAGCAAATGCGAAGTGTGTAAGCTGCTGAGCACAGAG
CTACAGCGCGAACTGAGTCGCACCGGTCGATCTCGAGAGGTGCTGGAGCTGGGGCAGGTGCT
GGATACAGGCAAGAGGAAGAGACACGTGCCTTACAGCGTTTCAGAGACAAGGCTGGAAGAGG
CCTTAGAGAATTTATGTGAGCGGATCCTGGACTATAGTGTTACGCTGAGCGCAAGGGCTCA
CTGAGATATGCCAAGGGTCAGAGTCAGACCATGGCAACACTGAAAGGCTAGTGAGAAGGG
GGTGAAGGTGGATCTGGGGATCCCTCTGGAGCTTTGGGATGAGCCAGCGTGGAGGTCACAT
ACCTCAAGAAGCAGTGTGAGACCATGTTGGAGGAGTTTGAAGACATTGTGGGAGACTGGTAC
TTCCACCATCAGGAGCAGCCCTACAAAATTTTCTCTGTGAAGGTGATGTGCTCCAGCTGC
TGAAACTGCATGTCTACAGGAACTTGGACTGGAAGGAGATCAGATGGGGAAGAGAAAA
CAGAAGGGGAGGAAGAGCAGGAGGAGGAGGAGGAAGAGGAGGAAGGAGGAGACAAG
ATGACCAAGACAGGAAGCCACCCAACTTGACCGAGAAGATCTTT**TGA**CCCTTGCCTTTGAG
CCCCCAGGAGGGGAAGGGATCATGGAGAGCCCTCTAAAGCTGCACTCTCCCTGCTCCACAG
CTTTCAGGGTGTGTTTATGAGTACTCCACCCAAGCTTGTAGCTGTTCTCTCCCATCTAACC
TCAGGCAAGATCCTGGTGAACAGCATGACATGGCTTCTGGGGTGGAGGGTGGGGGTGGAGG
TCCTGCTCCTAGAGATGAACTCTATCCAGCCCCCTTAATTGGCAGGTGTATGTGCTGACAGTA
CTGAAAGCTTTCTCTTTAACTGATCCACCCCCACCCAAAAGTCAGCAGTGGCACTGGAGC
TGTGGGCTTTGGGGAAGTCACTTAGCTCCTTAAGGTCTGTTTTTAGACCCTTCCAAGGAAGA
GGCCAGAACGGACATTCTCTGCGATCTATATACATTGCTGTATCCAGGAGGCTACACACCA
GCAAACCGTGAAGGAGAATGGGACACTGGGTCATGGCCTGGAGTTGCTGATAATTTAGGTGG
GATAGATACTTGGTCTACTTAAGCTCAATGTAACCCAGAGCCCACCATATAGTTTTATAGGT
GCTCAACTTTCTATATCGCTATTAAACTTTTTTCTTTTTTTCTA

FIGURE 28

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92256

><subunit 1 of 1, 248 aa, 1 stop

><MW: 28310, pI: 4.63, NX(S/T): 0

MGPVRLGILLFLFLAVHEAWAGMLKEEDDDTERLPSKCEVCKLLSTELQAELSRTGRSREVL
ELGQVLDTGKRKRHPVYSVSETRLEEALENLCERILDYSVHAERKGSRLRYAKGQSQTMATLK
GLVQKGVKVDLGIPLELWDEPSVEVTYLKKQCETMLEEFEDIVGDWYFHHQEQLQNFLCEG
HVLPAAEACIQTWTGKEITDGEKTEGEEEEEQEEEEEEEEEGDKMTKTGSHPKLDREDL

Important features of the protein:

Signal peptide:

amino acids 1-21

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 106-110

N-myristoylation site.

amino acids 115-121

Amidation site.

amino acids 70-74

FIGURE 29

AAGTACTTGTGTCCGGGTGGTGGACTGGATTAGCTGCGGAGCCCTGGAAGCTGCCTGTCCTT
CTCCCTGTGCTTAACCAGAGGTGCCCATGCGGTGGACAATGAGGCTGGTCACAGCAGCACTG
TTACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGCCCATGA
GGCCCTCTTGGACGAGGACACCCTCTTTTGGCAGGGCCTTGAAGTTTTCTACCCAGAGTTGG
GGAACATTGGCTGCAAGGTTGTTCTTGATTGTAACAACCTACAGACAGAAGTACCTCCTGG
ATGGAGCCGATAGTCAAGTTCCTGGGGGCGGTGGACGGCGCAACCTATATCCTGGTGATGGT
GGATCCAGATGCCCCTAGCAGAGCAGAACCAGACAGAGATTCTGGAGACATTGGCTGGTAA
CAGATATCAAGGGCGCCGACCTGAAGAAAGGAAGATTAGGGCCAGGAGTTATCAGCCTAC
CAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAGTTCTTTGTCTATCTTCA
GGAAGGAAAAGTCATCTCTCTCTTCCCAAGGAAAAAAAACCTCGAGGCTCTTGAAAAATGG
ACAGATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGCAAGCACCAGTTCATGACCCAG
AACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGGAAGGGCCAGCGAGCCCAAGCACAA
AACCAGGCAGAGATAGCTGCCTGCTAGATAGCCGGCTTTGCCATCCGGGCATGTGGCCACAC
TGCTCACCACCACGATGTGGGTATGGAACCCCTCTGGATACAGAACCCTTCTTTTCCAA
ATTAAAAAAAAAATCATCAA

FIGURE 30

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92274

><subunit 1 of 1, 223 aa, 1 stop

><MW: 25402, pI: 8.14, NX(S/T): 1

MGWTMRLVTAALLLGLMMVVTGDEDENSPCAHEALLDDETLFCQGLELVFYPELGNIGCKVVP
DCNNYRQKITSWMEPIVKFPGAVDGYIILVMVDPDAPSRAPRQRFWRHWLVTDIKGADLK
KGKIQGQELSAAYQAPSPPAHSGFHRYQFFVYLQEGKVISLLPENKTRGSWKMDRFLNRFHL
GEPEASTQFMTQNYQDSPTLQAPRGRASEPKHKTRQR

Important features of the protein:

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 169-173

Tyrosine kinase phosphorylation site.

amino acids 59-68

N-myristoylation sites.

amino acids 54-60, 83-89, 130-136

Phosphatidylethanolamine signature.

amino acids 113-157

FIGURE 31

GTGACCCACGCGTCCGAAGCTGCTGGAGCCACGATTTCAGTCCCCTGGACTGTAGATAAAGA
CCCTTTCTTGCCAGGTGCTGAGACAACCACACT**TATG**AGAGGCACTCCAGGAGACGCTGATGG
TGGAGGAAGGGCCGCTCTATCAATCAATCACTGTTGCTGTTATCACATGCAAGTATCCAGAGG
CTCTTGAGCAAGGCAGAGGGGATCCCATTTATTTGGGAATCCAGAATCCAGAAATGTGTTTG
TATTGTGAGAAGTTGGAGAACAGCCACATTGCAGCTAAAAGAGCAGAAGATCATGGATCT
GTATGGCCAACCCGAGCCCGTGAACCCCTTCCTTTTCTACCGTGCCAAGACTGGTAGGACCT
CCACCCCTTGAGTCTGTGGCCTTCCCGGACTGGTTCATTGCCCTCCTCCAAGAGAGACCAGCCC
ATCATTTCTGACTTCAGAACTTGGGAAGTCATACAACACTGCCTTTGAATTAATATAAATGA
CTGAACTCAGCCTAGAGGTGGCAGCTTGGTCTTTGTCTTAAAGTTTCTGGTTCCTCAATGTGT
TTTCGTCTACATTTTCTTAGTGTCAATTTTCACGCTGGTGCTGAGACAGGAGCAAGGCTGCTG
TTATCATCTCATTTTATAATGAAGAAGAAGCAATTACTTCATAGCAACTGAAGAACAGGATG
TGGCCTCAGAAGCAGGAGAGCTGGGTGGTATAAGGCTGTCCCTCTCAAGCTGGTGTGTGTAG
GCCACAAGGCATCTGCATGAGTGACTTTAAGACTCAAAGACCAAACTGAGCTTTCTTCTA
GGGGTGGGTATGAAGATGCTTCAGAGCTCATGCGCGTTACCCACGATGGCATGACTAGCACA
GAGCTGATCTCTGTTTCTGTTTGTCTTTATTCCTCTTGGGATGATATCATCCAGTCTTTAT
ATGTTGCCAATATACCTCATTGTGTGTAATAGAACCTTCTTAGCATTAAGACCTTGTAACA
AAAATAATTCTTGGGGTGGGTATGAAGATGCTTCAGAGCTCATGCGCGTTACCCACGATGGC
ATGACTAGCACAGAGCTGATCTCTGTTTCTGTTTGTCTTTATTCCTCTTGGGATGATATCA
TCCAGTCTTTATATGTTGCCAATATACCTCATTGTGTGTAATAGAACCTTCTTAGCATTAAG
ACCTTGTAACAACAAAATAATTCTGTGTAAAGTTAAATCATTTTTGTCCATAATTGTAATGTG
TAATCTTAAAGTTAAATAAACTTTGTGTATTTATATAATAATAAGCTAAAACGTATATAAA
ATAAAGAAAGAGTAAACTG

FIGURE 32

MRGTPGDADGGGRAVYQSITVAVITCKYPEALEQGRGDPYILGIQNPEMCLYCEKVGEQPTL
QLKEQKIMDLYGQPEPVKPELFYRAKTGRTSTLESVAFPDWFIASSKRDQPIILTSELGKSY
NTAFELNIND

Signal sequence:

amino acids 1-17

N-myristoylation site.

amino acids 10-16

Cell attachment sequence.

amino acids 36-39

FIGURE 33

GCGAGGCTGCACCAGCGCCTGGCACC**ATG**AGGACGCCTGGGCCTCTGCCCGTGTCTGTCTG
CTCCTGGCGGGAGCCCCGCGCGCGGCCCCACTCCCCGACCTGCTACTCCCGCATGCGGGC
CCTGAGCCAGGAGATCACCCGCGACTTCAACCTCCTGCAGGTCTCGGAGCCCTCGGAGCCAT
GTGTGAGATACCTGCCAGGCTGTACCTGGACATACACAATTACTGTGTGCTGGACAAGCTG
CGGGACTTTGTGGCCTCGCCCCCGTGTGGAAAGTGGCCAGGTAGATTCTTTGAAGGACAA
AGCAGGGAAGCTGTACACCATCATGAACTCGTTCTGCAGGAGAGATTTGGTATTCCTGTTGG
ATGACTGCAATGCCTTGGAATACCCAATCCCAGTGACTACGGTCCTGCCAGATCGTCAGCGC
TAAGGGAAGTGAAGCCAGAGAAAGAACCACAGAGAACTAAAGTTATGTCAGCTACCCAGACT
TAATGGGCCAGAGCCATGACCCCTCACAGGTCTTGTGTTAGTTGTATCTGAAACTGTTATGTA
TCTCTCTACCTTCTGGAAAACAGGGCTGGTATTCTACCCAGGAACCTCCTTTGAGCATAGA
GTTAGCAACCATGCTTCTCATTCCTTGACTCATGTCTTGCCAGGATGGTTAGATACACAGC
ATGTTGATTTGGTCACTAAAAGAAGAAAAGGACTAACAAGCTTCACTTTTATGAACAATA
TTTTGAGAACATGCACAATAGTATGTTTTTATTACTGGTTTAATGGAGTAATGGTACTTTTA
TTCCTTCTTGATAGAAACCTGCTTACATTTAACCAAGCTTCTATTATGCCTTTTCTAACAC
AGACTTTCTTCACTGTCTTTCATTTAAAAGAAATTAATGCTCTTAAGATATATATTTTACG
TAGTGCTGACAGGACCCACTCTTTCATTGAAAGGTGATGAAAATCAAATAAAGAATCTCTTC
ACATGGA

FIGURE 34

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA93011

><subunit 1 of 1, 136 aa, 1 stop

><MW: 15577, pI: 8.88, NX(S/T): 0

MRTPGPLPVLLLLLAGAPAAPPTPTCYSRMRALSQEITRDFNLLQVSEFSEPCVRYLPRLY
LDIHNYCVLDKLRDFVASPPCWKVAQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNALEY
IPVTTVLPRQR

Important features of the protein:

Signal peptide:

amino acids 1-19

Tyrosine kinase phosphorylation site.

amino acids 60-69

N-myristoylation site.

amino acids 16-22

FIGURE 35

GTCTCCGCGTCACAGGAACCTTCAGCACCCACAGGGCGGACAGCGCTCCCCTCTACCTGGAGA
CTTGACTCCCGCGCGCCCCAACCTTGCTTATCCCTTGACCGTCGAGTGTCAGAGATCCTGCA
GCCGCCAGTCCCGGCCCCCTCTCCCGCCCCACACCACCTCTCTGGCTCTTCTGTGTTTTAC
TCCTCCTTTTCATTATCATAACAAAAGCTACAGCTCCAGAGCCGAGCGCCGGGCTGTGACCCA
AGCCGAGCGTGAAGAATGGGGTTCCTCGGGACCGGCACTTGGATTCTGGTGTAGTGCTCC
CGATTCAAGCTTTCCCAAACCTGGAGGAAGCCAAGACAAATCTCTACATAATAGAGAATTA
AGTGCAGAAAGACCTTTGAATGAACAGATTGCTGAAGCAGAAGAAGACAAGATTAAAAAAC
ATATCCTCCAGAAAACAAGCCAGGTGAGAGCAACTATTCTTTTGTGATAACTTGAACCTGC
TAAAGGCAATAACAGAAAAGGAAAAAATTGAGAAAAGAAAGACAATCTATAAGAAGCTCCCCA
CTTGATAATAAGTTGAATGTGGAAGATGTTGATTCAACCAAGAATCGAAAACCTGATCGATGA
TTATGACTCTACTAAGAGTGGATTGGATCATAAATTTCAAGATGATCCAGATGGTCTTCATC
AACTAGACGGGACTCCTTTAACCGCTGAAGACATTGTCCATAAAATCGCTGCCAGGATTAT
GAAGAAAATGACAGAGCGGTGTTTGACAAGATTGTTCTAACTACTTAATCTCGGCCATTAT
CACAGAAAGCCAAGCACATACACTGGAAGATGAAGTAGCAGAGGTTTACAAAAATTAATCT
CAAAGGAAGCCAACAATTATGAGGAGGATCCCAATAAGCCCAAGCTGGACTGAGAATCAG
GCTGGAAAAATACCAGAGAAAGTGACTCCAATGGCAGCAATTCAGATGGTCTTGCTAAGGG
AGAAAACGATGAACAGTATCTAACACATTAACTTGACAATGGCTTGGAAGGAGAACTA
AAACCTACAGTGAAGACAACCTTGAGGAACTCCAATATTTCCCAAATTTCTATGCGCTACTG
AAAAGTATTGATTGAGAAAAGAAAGCAAAAGAGAAAGAAACACTGATTACTATCATGAAAAAC
ACTGATTGACTTTGTGAAGATGATGGTGAAATATGGAACAATATCTCCAGAAGAAGGTGTTT
CCTACCTTGAAAACCTTGGATGAAATGATTGCTCTTCAGACCAAAAACAAGCTAGAAAAAAT
GCTACTGACAAATATAAGCAAGCTTTTCCAGCACCATCAGAGAAGAGTCATGAAGAAACAGA
CAGTACCAAGGAAGAAGCAGCTAAGATGGAAGGAATATGGAAGCTTGAAGGATTCCACAA
AAGATGATAACTCCAACCCAGGAGGAAAGACAGATGAACCCAAAGGAAAAACAGAACCTAT
TTGGAAGCCATCAGAAAAAATATTGAATGGTTGAAGAAACATGACAAAAGGGAAATAAAGA
AGATTATGACCTTTCAAGATGAGAGACTTCATCAATAACAAGCTGATGCTTATGTGGAGA
AAGGCATCCTTGACAAGGAAGAAGCCGAGGCCATCAAGCGCATTTATAGCAGCCTGTAAAAA
TGGCAAAGATCCAGGAGTCTTTCACTGTTTCAGAAAACATAATATAGCTTAAACACTTC
TAATTCTGTGATTAATAATTTTTGACCCAAGGGTATTAGAAAGTGCTGAATTTACAGTAGT
TAACCTTTTACAAGTGTTAAAAACATAGCTTTCTTCCCGTAAAAACTATCTGAAAGTAAAGT
TGTATGTAAGCTGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGG

FIGURE 36

MGFLGTGTWILVLVLPIQAFPKPGGSQDKSLHNRELSAERPLNEQIAEAEEDKIKKTYPPEN
KPGQSNYSFVDNLNLLKAITEKEKIEKERQSISSPLDNKLNVEDVDSTKNRKLIDDYDSTK
SGLDHKFQDDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNGLLITESQA
HTLEDEVAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEVTPMAAIQDGLAKGENDET
VSNTLTLTNGLERRTKTYSEDNFEELQYFPNFIYALLKSIDSEKEAKEKETLITIMKTLIDFV
KMMVKYGTISPEEGVSYLENLDEMIALQTKNLEKNATDNISKLFPAPEKSEKHEETDSTKEE
AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYDLS
KMRDFINKQADAYVEKGILDKEEAIAIKRIYSSL

N-glycosylation sites:

amino acids 68-71, 346-349, 350-353

Casein kinase II phosphorylation site:

amino acids 70-73, 82-85, 97-100, 125-128, 147-150, 188-191, 217-
220, 265-268, 289-292, 305-308, 320-323, 326-329, 362-365, 368-
341, 369-372, 382-385, 386-389, 387-390

N-myristoylation sites:

amino acids 143-148, 239-244

FIGURE 37

GTTGCTCCGCGCGGCTCGGGGAGGGAGCCAGCAGCCTAGGGCCCTAGGCCCGGGCCACC**ATG**
 GCGCTGCCCTCCAGGCCAGCCGCCCTCCGGCACACACTGCTGCTCCTGCCAGCCCTTCTGAG
 CTCAGGTTGGGGGAGTTGGAGGCCACAAATAGATGGTCAGACCTGGGCTGAGCGGGCACTTC
 GGGAGAATGAACGCCACGCCTTCACTGCCGGGTGGCAGGGGGGCTGGCACCCCCAGATTG
 GCCTGGTATCTGGATGGACAGCTGCAGGAGGCCAGCACCTCAAGACTGCTGAGCCTGGGAGG
 GGAGGCCCTTCTTGGAGGCCACAGCACCTTCACTGTCACTGCCCATCGGGCCAGCATGAGC
 TCAACTGCTCTCTGCAGGACCCAGAAAGTGGCCGATCAGCCAACGCCCTGTGCATCCTTAAT
 GTGCAATTCAAGCCAGAGATTGCCCAAGTCGGCGCCAAGTACCAGGAAGCTCAGGGCCCCAGG
 CCTCCTGGTTGTCTCTTTGCCCCGGTGCGTGCCAAACCCGCGCGGCAATGTACCTGGATCG
 ACCAGGATGGGGCAGTGACTGTCAACACCTCTGACTTCCTGGTGTGGATGCCGAGAAGTAC
 CCCTGGCTCACCAACACACGGTGCAGCTGCAGCTCCGACGCCCTGGCACACAACCTCTCGGT
 GGTGGCCACCAATGACGTGGGTGTCAACAGTGCCTCGCTTCCAGCCCCAGGGCCCCCTCCGGC
 ACCCATCTCTGATATCAAGTGACTCCAACAACCTAAACCTCAACAACGTGCGCCTGCCACGG
 GAGAACATGTCCCTCCCGTCCAACCTTCAGCTCAATGACCTCACTCCAGATTCCAGAGCAGT
 GAAACCAAGACCCGGCAGATGGCTCAGAACAACAGCCGGCCAGAGCTTCTGGACCCGGAGC
 CCGCGCGCTCCTCACAGCCAAGGTTTCATCCGCCCTCCAGTGCTGGGCTATATCTATCGA
 GTGTCCAGCGTGAGCAGTGATGAGATCTGGCTC**TGAG**CCCGAGGGCGAGACAGGAGTATTCTC
 TTGGCCTCTGGACACCTCCCATTTCTCCAAAGGCATCCTTACCTAGCTAGGTACCAACGTT
 GAAGAAGTTATGCCACTGCCACTTTTGCTTGCCTCCTGGCTGGGGTGCCTCCATGTGCATG
 CACGTGAIGCATTTCACTGGGCTGTAACCCGACAGGGGCACAGGTATCTTTGGCAAGGCTACC
 AGTTGGAGCTAAGCCCCCTCATGCTGACTCAGGGTGGGCCCTGCATGTGATGACTGGGCCCTT
 CCAGAGGGAGCTCTTTGGCCAGGGGTGTTAGATGTCACTCCAGCATCCAAGTGTGGCATGGC
 CTGCTGTATACCCCAACCCAGTACTCCACAGCACCTTGTAAGTAGGCATGGGGCGTGCT
 GTGTGGGGACAGGGAGGGCCCTGCATGGATTTTCTCCTTCTTATGCTATGTAGCCTTTGTT
 CCTCAGTAAATTTAGGACCTTGCTAGCTGTGCAGAACCAATTGCCTTTGACAGAGAAA
 CCAACCCCTGACCCAGCGGTACCGGCCAAGCACAAACGTCCTTTTGTGTGCACACGTCTCTG
 CCCTTCACTTCTTCTCTTGTGCCACCTCCTCTTGGGAATTCTAGGTTACACGTTGGACC
 TTCTCTACTACTTCACTGGGCACTAGACTTTTCTATTGGCCTGTGCCATCGCCAGTATTAG
 CACAAGTTAGGGAGGAAGAGGCCAGGCGATGAGTCTAGTAGCACCCAGGACGGCTTGTAGCTA
 TGATCATTTTTCTACGGCGTTAGCACTTTAAGCACATCCCTAGGGGAGGGGTGAGTGAG
 GGGCCAGAGCCCTCTTTGTGGCTTCCCACGTTTGGCCTTCTGGGATTCACTGTGAGTGTCT
 CTGAGCTCTCGGGGTGATGGTTTTTCTCTCAGCATGTCTCTCCACCACGGGACCCAGGCC
 CTGACCAACCCATGGTTGCCTCATCAGCAGGAAGGTGCCCTTCTTGGAGGATGGTGCACACA
 GGCACATAATPCAACAGTGTGGAAGCTTTAGGGGAACATGGAGAAAGAGGAGACACATAC
 CCCAAAGTGACCTAAGAACACTTTAAAAGCAACATGTAATGATTGGAATTAATATAGTA
 CAGAATATATTTTCCCTTGTGTGAGATCTTCTTTGTAATGTTTTTCATGTTACTGCCTAGG
 GCGGTGCTGAGCACACAGCAAGTTTAATAAACTTGACTGAATTCATTTAAAAA
 AA
 AAAAAAAAAAAAAAAAAAAAAA

1000
 900
 800
 700
 600
 500
 400
 300
 200
 100
 0

FIGURE 38

MALPPGPAALRHLLLLPALLSSGWGELEPQIDGQTWAERALRENERHAFTCRVAGGPGTPR
LAWYLDGQLQEASTSRLLSVGGEAFSGGTSTFTVTAHRAQHELNCSLQDPRSGRSANASVIL
NVQFKPEIAQVGAKYQEAQGPGLLVVLFFALVRANPPANVTWIDQDGPVTVNTSDFLVLDAQN
YPWLTNHTVQLQLRSLAHNLSVVATNDVGVTASLPAPGPSRHPSLISSDSNNLKLNNVRLP
RENMSLPNLQLNDLTPDSRAVKPADRQMAQNNSRPELLDPEPGGLTSQGFIRLPVLGYIY
RVSSVSSEIWL

N-glycosylation sites:

amino acids 106-110, 119-123, 162-166, 175-179, 192-196, 205-209,
251-255, 280-284

Glycosaminoglycan attachment site:

amino acids 23-27

Casein kinase II phosphorylation sites:

amino acids 36-40, 108-112, 164-168, 282-286, 316-320

N-myristoylation sites:

amino acids 34-40, 89-95, 215-221, 292-298, 293-299

FIGURE 39

CGGGGACGGAAGCGGCCCTGGGCCCAGGGGCTGGAGCCGGGCCGGGGCG**ATG**TGGAGCGC
GGGCCGCGGCGGGGCTGCCCTGGCCGGTGCTGTTGGGGCTGCTGCTGGCGCTGTAGTGCCGG
GCGGTGGTGCCGCCAAGACCGGTGCGGAGCTCGTGACCTGCGGGTCGGTGCTGAAGCTGCTC
AATACGCACCACCGGTGCGGCTGCACTCGCACGACATCAAATACGGATCCGGCAGCGGCCA
GCAATCGGTGACCGGCGTAGAGCGTCGGACGACGCCAATAGCTACTGGCGGATCCGCGGCG
GCTCGGAGGGCGGGTGCCCGCGCGGGTCCCCGGTGCGCTGCGGGCAGGCGGTGAGGCTCACG
CATGTGCTTACGGGCAAGAACCTGCACACGCACCACTTCCCGTCGCCGCTGTCCAACAACCA
GGAGGTGAGTGCCCTTTGGGGAAGACGCGGAGGGCGACGACCTGGACCTATGGACAGTGCGCT
GCTCTGGACAGCACTGGGAGCGTGAGGCTGCTGTGCGCTTCCAGCATGTGGGCACCTCTGTG
TTCTGTCACTACGGGTGAGCAGTATGGAAGCCCCATCCGTGGGCAGCATGAGGTCCACGG
CATGCCCAGTGCCAAACACGCACAATACGTGGAAGGCCATGGAAGGCATCTTCATCAAGCCTA
GTGTGGAGCCCTCTGCAGGTACGATGAACT**TGA**GTGTGTGGATGGATGGGTGGATGGAGG
GTGGCAGGTGGGGCGTCTGCAGGGCCACTCTTGGCAGAGACTTTGGGTTGTAGGGGTCTC
AAGTGCCTTTGTGATTAAAGAATGTTGGTCTATGAAA

FIGURE 40

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96857
><subunit 1 of 1, 221 aa, 1 stop
><MW: 23598, pI: 6.96, NX(S/T): 0
MWSAGRGGAAWFVLLGLLLALLVPGGGAAGTGAELVTCGSVLKLLNTHHRVRLHSHDIKYGS
GSGQQSVTGVEASDDANSYWRIRGGSEGGCPRGSPVRCGQAVRLTHVLTGKNLTHHFPSPPL
SNNQEVSAFGEDGEGDDLTLWTVRCSGQHWEREAAVRFQHVGTSVFLSVTGEQYGSPIRGQH
EVHGMPSANTHNTWKAMEGIFIKPSVEPSAGHDEL
```

Important features of the protein:

Signal peptide:

amino acids 1-28

Glycosaminoglycan attachment site.

amino acids 62-66

N-myristoylation sites.

amino acids 16-22, 25-31, 27-33, 61-67, 71-77, 86-92, 87-93,
91-97, 190-196

Endoplasmic reticulum targeting sequence.

amino acids 218-223

FIGURE 41

GTTGCTATGTTGCCCAGGCTGGTCTTGAAGTGCCTTGACCTCCTAAAGTGTTGGAACCACAG
ACGTGAGCCACTCCACCCAGCCTAAAACCTTCATCTTCTTTGGATGAGATGAACACCTTTTAAC
AAGAGAACAGGACTCTATATAAATCGCTGTGGGCTCACCACCTCTAAGGAGGAGCACTGACT
GAAGACAGAAAAATTGATGAACTGAAGAAGACATGGTCCATTATGCCTTACAAACTTACACA
GTGCTTTGGGAATTCCAAAGTACTCAGTGGAGAGAGGTGTTTCAGGAGCCGTAGAGCCAGAT
CGTCATCATGTCTGCATTGTGGCTGCTGCTGGGCCTCCTTGCCCTGATGGACTTGTCTGAAA
GCAGCAACTGGGGATGCTATGGAACATCCAAAGCCTGGACACCCCTGGAGCATCTTGTGGG
ATTGGAAGACGTACGGCCTGAACTACTGTGGAGTTCGTGCTTCTGAAAGGCTGGCTGAAAT
AGACATGCCATACCTCCTGAAATATCAACCCATGATGCAAACCATTGGCCAAAAGTACTGCA
TGGATCCTGCCGTGATCGCTGGTGTCTTGCCAGGAAGTCTCCCGGTGACAAAATTCTGGTC
AACATGGGCGATAGGACTAGCATGGTGCAGGACCCCTGGCTCTCAAGCTCCCACATCCTGGAT
TAGTGAGTCTCAGGTTTCCCAGACAACTGAAGTCTGACTACTAGAATCAAAGAAATCCAGA
GGAGGTTTCCAACCTGGACCCCTGACCAGTACCTGAGAGGTGGACTCTGTGCCTACAGTGGG
GGTGCTGGCTATGTCCGAAGCAGCCAGGACCTGAGCTGTGACTTCTGCAATGATGTCCTTGC
ACGAGCCAAGTACCTCAAGAGACATGGCTTCTAACATCTCAGATGAAACCCCAAGACCATGAT
CACATATGCAGCCTCAAATGTTACACAGATAAAACTAGCCAAGGGCACCTGTAACCTGGGAAT
CTGAGTTTGACCTAAAAGTCATTAAAAATAACATGAATCCCATTAAAAAAAAAAAAAAAA

FIGURE 42

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96867

><subunit 1 of 1, 194 aa, 1 stop

><MW: 21431, pI: 8.57, NX(S/T): 0

MSALWLLGLLALMDLSESSNWGCYGNIQSLDTPGASCGIGRRHGLNYCGVRASERLAEIDM
PYLLKYQPMQTIGQKYCMDPAVIAGVLSRKSPGDKILVNMGDRTSMVQDPGSQAPTSWISE
SQVSQTTEVLTTRIKEIQRRFPTWTPDQYLRGGLCAYSGGAGYVRSSQDLSCDFCNDVLARA
KYLKRHGF

Important features of the protein:

Signal peptide:

amino acids 1-19

N-myristoylation sites.

amino acids 23-29, 26-32, 35-41, 45-51, 50-56, 76-82, 156-162

Amidation site.

amino acids 40-44

FIGURE 43

TTGAAAATCTACTCTATCAGCTGCTGTGGTTGCCACCATTCTCAGGACCCTCGCC**ATG**AAAG
CCCTTATGCTGCTCACCTGTCTGTCTGTCTGCTGGGTCTCAGCTGACATTGCTGTAC
TCCTGCTACAAGGTCCTGTGCTGGGCTGTGTGGACCGGCAGTCTGCCGCCCTGGAGCCAGG
ACAGCAATGCCTGACAACACATGCATACCTTGGTAAGATGTGGGTTTTCTCCAATCTGCGCT
GTGGCACACCAGAAGAGCCCTGTCAGGAGGCCTTCAACCAAACCAACCGCAAGCTGGGTCTG
ACATATAACACCACCTGCTGCAACAAGGACAACTGCAACAGCGCAGGACCCCGGCCACTCC
AGCCCTGGGCCTTGCTTTCCTTACCTCCTTGCGCTGGCCTTGGCCTCTGGCTGCTGCAC**TGAG**
ACTCATTTCCATTGGCTGCCCTCCTCCACCTGCCTTGGCCTGAGCCTCTCTCCCTGTGTCT
CTGTATCCCTGGCCTTACAGAATCGTCTCTCCCTAGCTCCCATTTCTTTAATTAACACTG
TTCCGAGTGGTCTCCTCATCCATCCTTCCCACCTCACACCCCTTCACTCTCCTTTTTCTGGGT
CCCTTCCCCTTCCCTTCCAGGACCTCCATTGGCTCCTAGAAGGGCTCCCCACTTTGCTTCCT
ATACTCTGCTGTCCCCTACTTGAGGAGGGATTGGGATCTGGGCCTGAAATGGGGCTTCTGTG
TTGTCCCAGTGAAGGCTCCCAAGGACCTGATGACCTCACTGTACAGAGCTGACTCCCCA
AACCAGGCTCCCATATGTACCCATCCCCATACTCACCTCTTCCATTTGAGTAATAAA
TGCTGAGTCTGGAAAAAAAAAAAAAAAAA

FIGURE 44

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96878
><subunit 1 of 1, 125 aa, 1 stop
><MW: 13821, pI: 8.60, NX(S/T): 2
MKALMLLTLSVLLCWVSADIRCHSCYKVPVLGCVDRQSCRLEPGQQCLTHAYLGKMWVFSN
LRCGTPEEPCQEAFNQTNRKLGITYNTCCNKDNCNSAGPRPTPALGLVFLTSLAGLGLWLLH

Important features of the protein:

Signal peptide:

amino acids 1-18

N-glycosylation sites.

amino acids 77-81, 88-92

N-myristoylation site.

amino acids 84-90

Ly-6 / u-PAR domain protein signature.

amino acids 85-98

FIGURE 45

ACGGGCCGCGAGCGGCAGTGACGTAGGGTTGGCGCACGGATCCGTTGCGGCTGCAGCTCTGCA
GTCGGGGCGTTCCCTTCGCGCCGCCAGGGGTAGCGGTGTAGCTGCGCAGCGTCGCGCGCGCT
ACCGCACCCAGGTTGGGCCGTAGGCGCTTGGCAGCCCGCGCCATCTTCATCGAGCGCCAT
GGCCGCGAGCTGCGGGCCGGGAGCGGGCCGGTACTGCTTGCTCCTCGGCTTGCAATTTGTTTC
TGCTGACCGGGGCCCTGCCTGGGCTGGAACGACCTGCAGAAATGTTGCTGCGGGATGTA
AAAGCTCTTACCCTCCACTATGACCGCTATACCACCTCCCGCAGGCTGGATCCCATCCCACA
GTTGAAATGTGTTGGAGGCACAGCTGGTTGTGATTCTTATACCCCAAAAGTCATACAGTGTC
AGAACAAAGGCTGGGATGGGTATGATGTACAGTGGGAATGTAAGACGGACTTAGATATTGCA
TACAAATTTGGAAAACTGTGGTGAGCTGTGAAGCTATGAGTCCTCTGAAGACCAATGATGT
ACTAAGAGGTTCTTGTTGGCTTGGAGTATAATTTAGATTATACAGAACTTGGCCTGCAGAAAC
TGAAGGAGTCTGGAAAGCAGCACGGCTTTGCCTCTTCTCTGATTATTATTATAAGTGGTCC
TCGGCGGATTCTGTAAACATGAGTGGATTGATTACCATCGTGGTACTCCTTGGGATCGCCTT
TGTAAGCTATAAGCTGTTCTGAGTGACGGGCAGTATTCTCCTCCACCGTACTCTGAGTATC
CTCCATTTTCCCACCGTTACCAGAGATTACCAACTCAGCAGGACCTCCTCCCCAGGCTTT
AAGCTGAGTTTACAGGACCACAGAATACTGGCCATGGTGCAACTTCTGGTTTGGCAGTG
TTTTACAGGACAACAAGGATATGAAAATTCAGGACCAGGTTCTGGACAGGCTTGGGAAGTG
GTGGAATACTAGGATATTTGTTTGGCAGCAATAGAGCGGCAACACCCTTCTCAGACTCGTGG
TACTACCCGTCCTATCCTCCCTCTACCTGGCACGTGGAATAGGGCTTACTACCCCTTCA
TGGAGGCTCGGGCAGCTATTCCGTATGTTCAAACCTCAGACACGAAAACAGAACTGCATCAG
GATATGTTGGTACCAGGAGACGATTAAGTAGAAAGTTGGAGTCAAACACTGGATGCAGAAAT
TTTGGATTTTTCATCACTTCTCTTTAGAAAAAAGTACTACCTGTTAAACATTTGGAAAAAG
GGGATATTCAAAGTTCTGTGGTGTATGTCCAGTGTAGCTTTTTGTATTCTATTATTTGAG
GCTAAAAGTTGATGTGTGACAAAATACTTATGTGTGTATGTGAGTGAACATGCAGATGTA
TATTGCAGTTTTTGAAGTGATCATTACTGTGGAATGCTAAAAATACATTAATTTCTAAAC
CTGTGATGCCCTAAGAAGCATTAAGAATGAAGGTGTTGTACTAATAGAACTAAGTACAGAA
AATTTAGTTTTAGTGGTTGTAGCTGATGAGTTATTACCTCATAGAGACTATAATATTCTA
TTTGGTATTATATTATTGATGTTTGTGTTCTTCAAACATTTAAATCAAGCTTTGGACTAA
TTATGCTAATTTGTGAGTTCTGATCACTTTTGAGCTCTGAAGCTTTGAATCATTAGTGGTG
GAGATGGCCTTCTGGTAACTGAATATTACCTTCTGTAGGAAAAGGTGAAAAATAAGCATCTA
GAAGGTGTTGTGAATGACTCTGTGCTGGCAAAATGCTTGAAACCTCTATATTCTTTCGT
TCATAAGAGGTAAGGTCAAATTTTTCAACAAAAGTCTTTTAATAACAAAAGCATGCAGTTC
TCTGTGAAATCTCAAATATTGTTGTAATAGTCTGTTTCAATCTTAAAAAGAAATCA

FIGURE 46

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96889
><subunit 1 of 1, 339 aa, 1 stop
><MW: 36975, pI: 7.85, NX(S/T): 1
MAAACGPGAAGYCLLLGLHLFLLTAGPALGWNDPDRMLLRDVKALTLHYDRYTTSRRLDPIP
QLKCVGGTAGCDSYTPKVIQCQNGWDGYDVQWECKTDLDIAYKFGKTVVSCEGYESSEDQY
VLRGSCGLEYNLDYTELGQLKLGESGKQHGFAFSDYKKWSSADSCNMSGLITIVVLLGIA
FVVYKFLFLSDGQYSPPPYSEYPPFESHRYQRFTNSAGPPPPGFKSEFTGPQNTGHGATSGFGS
AFTGQQGYENSGPGFWTGLGTGGILGYLFGSNRAATPFSDSWYYPSYPPSYPGTWNRAYSPL
HGGSGSYSVCSNSDTKTRTASGYGGTRRR
```

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 171-190

N-glycosylation site.

amino acids 172-176

Glycosaminoglycan attachment sites.

amino acids 244-248, 259-263, 331-335

Tyrosine kinase phosphorylation site.

amino acids 98-106

N-myristoylation sites.

amino acids 68-74, 69-75, 131-137, 241-247, 247-253, 266-272,
270-276, 278-284, 312-318